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<120> VIRAL VECTORS ENCODING APOPTOSIS-INDUCING PROTEINS AND
METHODS FOR MAKING AND USING THE SAME

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<140> Not Yet Assigned

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<150> 60/134,416

<151> 1999-05-17

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<170> PatentIn Ver. 2.0

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<211> 1890

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (189)..(1034)

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cctcagcctc tacaggactg agaagaagta aaaccgtttg ctgggggtgg cctgactcac 180

cagctgcc atg cag cag ccc ttc aat tac cca tat ccc cag atc tac tgg 230

Met Gln Gln Pro Phe Asn Tyr Pro Tyr Pro Gln Ile Tyr Trp

1

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10

gtg gac agc agt gcc agc tct ccc tgg gcc cct cca ggc aca gtt ctt 278

Val Asp Ser Ser Ala Ser Ser Pro Trp Ala Pro Pro Gly Thr Val Leu

15

20

25

30

ccc tgt cca acc tct gtg ccc aga agg cct ggt caa agg agg cca cca 326

Pro Cys Pro Thr Ser Val Pro Arg Arg Pro Gly Gln Arg Arg Pro Pro

35

40

45

cca cca ccg cca ccg cca cca cta cca cct ccg ccg ccg ccg cca cca 374

Pro Pro Pro Pro Pro Pro Pro Pro Leu Pro Pro Pro Pro Pro Pro Pro

50

55

60

ctg cct cca cta ccg ctg cca ccc ctg aag aag aga ggg aac cac agc 422

Leu Pro Pro Leu Pro Leu Pro Pro Leu Lys Lys Arg Gly Asn His Ser

65

70

75

aca ggc ctg tgt ctc ctt gtg atg ttt ttc atg gtt ctg gtt gcc ttg 470

Thr Gly Leu Cys Leu Leu Val Met Phe Phe Met Val Leu Val Ala Leu

80

85

90

gta gga ttg ggc ctg ggg atg ttt cag ctc ttc cac cta cag aag gag 518

Val Gly Leu Gly Leu Gly Met Phe Gln Leu Phe His Leu Gln Lys Glu

95

100

105

110

ctg gca gaa ctc cga gag tct acc agc cag atg cac aca gca tca tct 566

Leu Ala Glu Leu Arg Glu Ser Thr Ser Gln Met His Thr Ala Ser Ser

115

120

125

ttg gag aag caa ata ggc cac ccc agt cca ccc cct gaa aaa aag gag 614

Leu Glu Lys Gln Ile Gly His Pro Ser Pro Pro Pro Glu Lys Lys Glu

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 acaaat 1890

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 <212> PRT
 <213> Homo sapiens

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 Pro Thr Ser Val Pro Arg Arg Pro Gly Gln Arg Arg Pro Pro Pro Pro
 35 40 45
 Pro Pro Pro Pro Pro Leu Pro Pro Pro Pro Pro Pro Pro Leu Pro
 50 55 60
 Pro Leu Pro Leu Pro Pro Leu Lys Lys Arg Gly Asn His Ser Thr Gly
 65 70 75 80
 Leu Cys Leu Leu Val Met Phe Phe Met Val Leu Val Ala Leu Val Gly
 85 90 95
 Leu Gly Leu Gly Met Phe Gln Leu Phe His Leu Gln Lys Glu Leu Ala
 100 105 110

Glu Leu Arg Glu Ser Thr Ser Gln Met His Thr Ala Ser Ser Leu Glu
 115 120 125

Lys Gln Ile Gly His Pro Ser Pro Pro Pro Glu Lys Lys Glu Leu Arg
 130 135 140

Lys Val Ala His Leu Thr Gly Lys Ser Asn Ser Arg Ser Met Pro Leu
 145 150 155 160

Glu Trp Glu Asp Thr Tyr Gly Ile Val Leu Leu Ser Gly Val Lys Tyr
 165 170 175

Lys Lys Gly Gly Leu Val Ile Asn Glu Thr Gly Leu Tyr Phe Val Tyr
 180 185 190

Ser Lys Val Tyr Phe Arg Gly Gln Ser Cys Asn Asn Leu Pro Leu Ser
 195 200 205

His Lys Val Tyr Met Arg Asn Ser Lys Tyr Pro Gln Asp Leu Val Met
 210 215 220

Met Glu Gly Lys Met Met Ser Tyr Cys Thr Thr Gly Gln Met Trp Ala
 225 230 235 240

Arg Ser Ser Tyr Leu Gly Ala Val Phe Asn Leu Thr Ser Ala Asp His
 245 250 255

Leu Tyr Val Asn Val Ser Glu Leu Ser Leu Val Asn Phe Glu Glu Ser
 260 265 270

Gln Thr Phe Phe Gly Leu Tyr Lys Leu
 275 280

<210> 7

<211> 1623

<212> DNA

<213> Rattus norvegicus

<220>

<221> CDS

<222> (74)..(910)

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 Met Gln Gln Pro Val Asn Tyr Pro Cys Pro Gln Ile

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tac	tgg	gta	gac	agc	agt	gcc	act	tct	cct	tgg	gct	cct	cca	ggg	tca	157									
Tyr	Trp	Val	Asp	Ser	Ser	Ala	Thr	Ser	Pro	Trp	Ala	Pro	Pro	Gly	Ser										
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gtt	ttt	tct	tgt	cca	tcc	tct	ggg	cct	aga	ggg	cca	gga	caa	agg	aga	205									
Val	Phe	Ser	Cys	Pro	Ser	Ser	Gly	Pro	Arg	Gly	Pro	Gly	Gln	Arg	Arg										
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cca	ccg	cct	cca	cca	cca	cct	cca	tca	cca	cta	cca	ccg	cct	tcc	caa	253									
Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Ser	Pro	Leu	Pro	Pro	Pro	Ser	Gln										
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cca	ccc	ccg	ctg	cct	cca	cta	agc	cct	cta	aag	aag	aag	gac	aac	ata	301									
Pro	Pro	Pro	Leu	Pro	Pro	Leu	Ser	Pro	Leu	Lys	Lys	Lys	Asp	Asn	Ile										
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Glu	Leu	Trp	Leu	Pro	Val	Ile	Phe	Phe	Met	Val	Leu	Val	Ala	Leu	Val										
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95					100					105															
gca	gaa	ctc	cgt	gag	ttc	acc	aac	cac	agc	ctt	aga	gta	tca	tct	ttt	445									
Ala	Glu	Leu	Arg	Glu	Phe	Thr	Asn	His	Ser	Leu	Arg	Val	Ser	Ser	Phe										
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gaa	aag	caa	ata	gcc	aac	ccc	agc	aca	ccc	tct	gaa	acc	aaa	aag	cca	493									
Glu	Lys	Gln	Ile	Ala	Asn	Pro	Ser	Thr	Pro	Ser	Glu	Thr	Lys	Lys	Pro										
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Arg	Ser	Val	Ala	His	Leu	Thr	Gly	Asn	Pro	Arg	Ser	Arg	Ser	Ile	Pro										
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Tyr	Lys	Lys	Gly	Gly	Leu	Val	Ile	Asn	Glu	Ala	Gly	Leu	Tyr	Phe	Val										
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tat	tcc	aaa	gta	tac	ttc	cgg	ggt	cag	tct	tgc	aac	agc	cag	ccc	cta	685									
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agc cac aag gtc tat atg agg aac ttt aag tat cct ggg gat ctg gtg			733
Ser His Lys Val Tyr Met Arg Asn Phe Lys Tyr Pro Gly Asp Leu Val			
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cta atg gag gag aag aag ttg aat tac tgc act act ggc cag ata tgg			781
Leu Met Glu Glu Lys Lys Leu Asn Tyr Cys Thr Thr Gly Gln Ile Trp			
	225	230	235
gcc cac agc agc tac cta ggg gca gta ttt aat ctt acc gtt gct gac			829
Ala His Ser Ser Tyr Leu Gly Ala Val Phe Asn Leu Thr Val Ala Asp			
	240	245	250
cat tta tat gtc aac ata tct caa ctc tct ctg atc aat ttt gag gaa			877
His Leu Tyr Val Asn Ile Ser Gln Leu Ser Leu Ile Asn Phe Glu Glu			
	255	260	265
tct aag acc ttt ttt ggc tta tat aag ctt taa aggaaaaagc attttagaat			930
Ser Lys Thr Phe Phe Gly Leu Tyr Lys Leu			
270	275		
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<210> 8

<211> 278

<212> PRT

<213> Rattus norvegicus

<400> 8

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Pro Ser Ser Gly Pro Arg Gly Pro Gly Gln Arg Arg Pro Pro Pro Pro
35 40 45

Pro Pro Pro Pro Ser Pro Leu Pro Pro Pro Ser Gln Pro Pro Pro Leu
50 55 60

Pro Pro Leu Ser Pro Leu Lys Lys Lys Asp Asn Ile Glu Leu Trp Leu
65 70 75 80

Pro Val Ile Phe Phe Met Val Leu Val Ala Leu Val Gly Met Gly Leu
85 90 95

Gly Met Tyr Gln Leu Phe His Leu Gln Lys Glu Leu Ala Glu Leu Arg
100 105 110

Glu Phe Thr Asn His Ser Leu Arg Val Ser Ser Phe Glu Lys Gln Ile
115 120 125

Ala Asn Pro Ser Thr Pro Ser Glu Thr Lys Lys Pro Arg Ser Val Ala
130 135 140

His Leu Thr Gly Asn Pro Arg Ser Arg Ser Ile Pro Leu Glu Trp Glu
145 150 155 160

Asp Thr Tyr Gly Thr Ala Leu Ile Ser Gly Val Lys Tyr Lys Lys Gly
165 170 175

Gly Leu Val Ile Asn Glu Ala Gly Leu Tyr Phe Val Tyr Ser Lys Val
180 185 190

Tyr Phe Arg Gly Gln Ser Cys Asn Ser Gln Pro Leu Ser His Lys Val
195 200 205

Tyr Met Arg Asn Phe Lys Tyr Pro Gly Asp Leu Val Leu Met Glu Glu
210 215 220

Lys Lys Leu Asn Tyr Cys Thr Thr Gly Gln Ile Trp Ala His Ser Ser

225	230	235	240
Tyr Leu Gly Ala Val Phe Asn Leu Thr Val Ala Asp His Leu Tyr Val			
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Asn Ile Ser Gln Leu Ser Leu Ile Asn Phe Glu Glu Ser Lys Thr Phe			
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Phe Gly Leu Tyr Lys Leu			
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<210> 9
 <211> 1707
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (125)..(964)

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tgcc atg cag cag ccc atg aat tac cca tgt ccc cag atc ttc tgg gta	169
Met Gln Gln Pro Met Asn Tyr Pro Cys Pro Gln Ile Phe Trp Val	
1 5 10 15	

gac agc agt gcc act tca tct tgg gct cct cca ggg tca gtt ttt ccc	217
Asp Ser Ser Ala Thr Ser Ser Trp Ala Pro Pro Gly Ser Val Phe Pro	
20 25 30	

tgt cca tct tgt ggg cct aga ggg ccg gac caa agg aga ccg cca cct	265
Cys Pro Ser Cys Gly Pro Arg Gly Pro Asp Gln Arg Arg Pro Pro Pro	
35 40 45	

cca cca cca cct gtg tca cca cta cca ccg cca tca caa cca ctc cca	313
Pro Pro Pro Pro Val Ser Pro Leu Pro Pro Pro Ser Gln Pro Leu Pro	
50 55 60	

ctg ccg cca ctg acc cct cta aag aag aag gac cac aac aca aat ctg	361
Leu Pro Pro Leu Thr Pro Leu Lys Lys Lys Asp His Asn Thr Asn Leu	
65 70 75	

tgg cta ccg gtg gta ttt ttc atg gtt ctg gtg gct ctg gtt gga atg	409
Trp Leu Pro Val Val Phe Phe Met Val Leu Val Ala Leu Val Gly Met	

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gga tta gga atg tat cag ctc ttc cac ctg cag aag gaa ctg gca gaa				457
Gly Leu Gly Met Tyr Gln Leu Phe His Leu Gln Lys Glu Leu Ala Glu				
	100	105	110	
ctc cgt gag ttc acc aac caa agc ctt aaa gta tca tct ttt gaa aag				505
Leu Arg Glu Phe Thr Asn Gln Ser Leu Lys Val Ser Ser Phe Glu Lys				
	115	120	125	
caa ata gcc aac ccc agt aca ccc tct gaa aaa aaa gag ccg agg agt				553
Gln Ile Ala Asn Pro Ser Thr Pro Ser Glu Lys Lys Glu Pro Arg Ser				
	130	135	140	
gtg gcc cat tta aca ggg aac ccc cac tca agg tcc atc cct ctg gaa				601
Val Ala His Leu Thr Gly Asn Pro His Ser Arg Ser Ile Pro Leu Glu				
	145	150	155	
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Trp Glu Asp Thr Tyr Gly Thr Ala Leu Ile Ser Gly Val Lys Tyr Lys				
160	165	170	175	
aaa ggt ggc ctt gtg atc aac gaa act ggg ttg tac ttc gtg tat tcc				697
Lys Gly Gly Leu Val Ile Asn Glu Thr Gly Leu Tyr Phe Val Tyr Ser				
	180	185	190	
aaa gta tac ttc cgg ggt cag tct tgc aac aac cag ccc cta aac cac				745
Lys Val Tyr Phe Arg Gly Gln Ser Cys Asn Asn Gln Pro Leu Asn His				
	195	200	205	
aag gtc tat atg agg aac tct aag tat cct gag gat ctg gtg cta atg				793
Lys Val Tyr Met Arg Asn Ser Lys Tyr Pro Glu Asp Leu Val Leu Met				
	210	215	220	
gag gag aag agg ttg aac tac tgc act act gga cag ata tgg gcc cac				841
Glu Glu Lys Arg Leu Asn Tyr Cys Thr Thr Gly Gln Ile Trp Ala His				
	225	230	235	
agc agc tac ctg ggg gca gta ttc aat ctt acc agt gct gac cat tta				889
Ser Ser Tyr Leu Gly Ala Val Phe Asn Leu Thr Ser Ala Asp His Leu				
240	245	250	255	
tat gtc aac ata tct caa ctc tct ctg atc aat ttt gag gaa tct aag				937
Tyr Val Asn Ile Ser Gln Leu Ser Leu Ile Asn Phe Glu Glu Ser Lys				
	260	265	270	
acc ttt ttc ggc ttg tat aag ctt taa aagaaaaagc attttaaaat				984
Thr Phe Phe Gly Leu Tyr Lys Leu				

gatctactat tctttatcat gggcaccagg aatattgtct tgaatgagag tcttcttaag 1044
acctattgag attaattaag actacatgag ccacaaagac ctcatgaccg caagggtccaa 1104
cagggtcagct atccttcatt ttctcgaggt ccatggagtg gtccttaatg cctgcatcat 1164
gagccagatg gaaggaggtc tgtgactgag ggacataaag ctttgggctg ctgtgtgaca 1224
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agagcaaaca gattctaagg agtcatataa ataaaatatg tacattatgg agtacatatt 1644
agaaacctgt tacatttgat gctagatatt tgaatgtttc ttggcaataa actctaatag 1704
tct 1707

<210> 10

<211> 279

<212> PRT

<213> Mus musculus

<400> 10

Met Gln Gln Pro Met Asn Tyr Pro Cys Pro Gln Ile Phe Trp Val Asp

1

5

10

15

Ser Ser Ala Thr Ser Ser Trp Ala Pro Pro Gly Ser Val Phe Pro Cys

20

25

30

Pro Ser Cys Gly Pro Arg Gly Pro Asp Gln Arg Arg Pro Pro Pro Pro

35

40

45

Pro Pro Pro Val Ser Pro Leu Pro Pro Pro Ser Gln Pro Leu Pro Leu

50

55

60

Pro Pro Leu Thr Pro Leu Lys Lys Lys Asp His Asn Thr Asn Leu Trp

65	70	75	80
Leu Pro Val Val Phe Phe Met Val Leu Val Ala Leu Val Gly Met Gly	85	90	95
Leu Gly Met Tyr Gln Leu Phe His Leu Gln Lys Glu Leu Ala Glu Leu	100	105	110
Arg Glu Phe Thr Asn Gln Ser Leu Lys Val Ser Ser Phe Glu Lys Gln	115	120	125
Ile Ala Asn Pro Ser Thr Pro Ser Glu Lys Lys Glu Pro Arg Ser Val	130	135	140
Ala His Leu Thr Gly Asn Pro His Ser Arg Ser Ile Pro Leu Glu Trp	145	150	155
Glu Asp Thr Tyr Gly Thr Ala Leu Ile Ser Gly Val Lys Tyr Lys Lys	165	170	175
Gly Gly Leu Val Ile Asn Glu Thr Gly Leu Tyr Phe Val Tyr Ser Lys	180	185	190
Val Tyr Phe Arg Gly Gln Ser Cys Asn Asn Gln Pro Leu Asn His Lys	195	200	205
Val Tyr Met Arg Asn Ser Lys Tyr Pro Glu Asp Leu Val Leu Met Glu	210	215	220
Glu Lys Arg Leu Asn Tyr Cys Thr Thr Gly Gln Ile Trp Ala His Ser	225	230	235
Ser Tyr Leu Gly Ala Val Phe Asn Leu Thr Ser Ala Asp His Leu Tyr	245	250	255
Val Asn Ile Ser Gln Leu Ser Leu Ile Asn Phe Glu Glu Ser Lys Thr	260	265	270
Phe Phe Gly Leu Tyr Lys Leu	275		

<210> 11

<211> 2534

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (195)..(1202)

<400> 11

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ggcactggca cggaacacac cctgaggcca gccctggctg cccaggcgga gctgcctctt 120

ctcccgcggg ttggtggacc cgctcagtag ggagttgggg aagctctttc acttcggagg 180

attgctcaac aacc atg ctg ggc atc tgg acc ctc cta cct ctg gtt ctt 230

Met Leu Gly Ile Trp Thr Leu Leu Pro Leu Val Leu

1

5

10

acg tct gtt gct aga tta tgc tcc aaa agt gtt aat gcc caa gtg act 278

Thr Ser Val Ala Arg Leu Ser Ser Lys Ser Val Asn Ala Gln Val Thr

15

20

25

gac atc aac tcc aag gga ttg gaa ttg agg aag act gtt act aca gtt 326

Asp Ile Asn Ser Lys Gly Leu Glu Leu Arg Lys Thr Val Thr Thr Val

30

35

40

gag act cag aac ttg gaa ggc ctg cat cat gat ggc caa ttc tgc cat 374

Glu Thr Gln Asn Leu Glu Gly Leu His His Asp Gly Gln Phe Cys His

45

50

55

60

aag ccc tgt cct cca ggt gaa agg aaa gct agg gac tgc aca gtc aat 422

Lys Pro Cys Pro Pro Gly Glu Arg Lys Ala Arg Asp Cys Thr Val Asn

65

70

75

ggg gat gaa cca gac tgc gtg ccc tgc caa gaa ggg aag gag tac aca 470

Gly Asp Glu Pro Asp Cys Val Pro Cys Gln Glu Gly Lys Glu Tyr Thr

80

85

90

gac aaa gcc cat ttt tct tcc aaa tgc aga aga tgt aga ttg tgt gat 518

Asp Lys Ala His Phe Ser Ser Lys Cys Arg Arg Cys Arg Leu Cys Asp

95

100

105

gaa gga cat ggc tta gaa gtg gaa ata aac tgc acc cgg acc cag aat 566

Glu Gly His Gly Leu Glu Val Glu Ile Asn Cys Thr Arg Thr Gln Asn

110

115

120

acc aag tgc aga tgt aaa cca aac ttt ttt tgt aac tct act gta tgt 614

Thr Lys Cys Arg Cys Lys Pro Asn Phe Phe Cys Asn Ser Thr Val Cys

125

130

135

140

gaa cac tgt gac cct tgc acc aaa tgt gaa cat gga atc atc aag gaa 662

Glu His Cys Asp Pro Cys Thr Lys Cys Glu His Gly Ile Ile Lys Glu

145	150	155	
tgc aca ctc acc agc aac acc aag tgc aaa gag gaa gga tcc aga tct			710
Cys Thr Leu Thr Ser Asn Thr Lys Cys Lys Glu Glu Gly Ser Arg Ser			
160	165	170	
aac ttg ggg tgg ctt tgt ctt ctt ctt ttg cca att cca cta att gtt			758
Asn Leu Gly Trp Leu Cys Leu Leu Leu Leu Pro Ile Pro Leu Ile Val			
175	180	185	
tgg gtg aag aga aag gaa gta cag aaa aca tgc aga aag cac aga aag			806
Trp Val Lys Arg Lys Glu Val Gln Lys Thr Cys Arg Lys His Arg Lys			
190	195	200	
gaa aac caa ggt tct cat gaa tct cca acc tta aat cct gaa aca gtg			854
Glu Asn Gln Gly Ser His Glu Ser Pro Thr Leu Asn Pro Glu Thr Val			
205	210	215	220
gca ata aat tta tct gat gtt gac ttg agt aaa tat atc acc act att			902
Ala Ile Asn Leu Ser Asp Val Asp Leu Ser Lys Tyr Ile Thr Thr Ile			
225	230	235	
gct gga gtc atg aca cta agt caa gtt aaa ggc ttt gtt cga aag aat			950
Ala Gly Val Met Thr Leu Ser Gln Val Lys Gly Phe Val Arg Lys Asn			
240	245	250	
ggc gtc aat gaa gcc aaa ata gat gag atc aag aat gac aat gtc caa			998
Gly Val Asn Glu Ala Lys Ile Asp Glu Ile Lys Asn Asp Asn Val Gln			
255	260	265	
gac aca gca gaa cag aaa gtt caa ctg ctt cgt aat tgg cat caa ctt			1046
Asp Thr Ala Glu Gln Lys Val Gln Leu Leu Arg Asn Trp His Gln Leu			
270	275	280	
cat gga aag aaa gaa gcg tat gac aca ttg att aaa gat ctc aaa aaa			1094
His Gly Lys Lys Glu Ala Tyr Asp Thr Leu Ile Lys Asp Leu Lys Lys			
285	290	295	300
gcc aat ctt tgt act ctt gca gag aaa att cag act atc atc ctc aag			1142
Ala Asn Leu Cys Thr Leu Ala Glu Lys Ile Gln Thr Ile Ile Leu Lys			
305	310	315	
gac att act agt gac tca gaa aat tca aac ttc aga aat gaa atc caa			1190
Asp Ile Thr Ser Asp Ser Glu Asn Ser Asn Phe Arg Asn Glu Ile Gln			
320	325	330	
agc ttg gtc tag agtgaaaaac aacaaattca gttctgagta tatgcaatta			1242
Ser Leu Val			

gtgtttgaaa agattcttaa tagctggctg taaatactgc ttggtttttt actgggtaca 1302
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 taggaattgc tcttgtcata ccotcaagtt tctaagattt aagattctcc ttactactat 2322
 cctacgttta aatatctttg aaagtttgta ttaaatgtga attttaagaa ataatttta 2382
 tatttctgta aatgtaaact gtgaagatag ttataaactg aagcagatac ctggaaccac 2442
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 aggtaaaagt acgtaattaa ataatgtttt tg 2534

<211> 335

<212> PRT

<213> Homo sapiens

<400> 12

Met Leu Gly Ile Trp Thr Leu Leu Pro Leu Val Leu Thr Ser Val Ala
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Arg Leu Ser Ser Lys Ser Val Asn Ala Gln Val Thr Asp Ile Asn Ser
20 25 30

Lys Gly Leu Glu Leu Arg Lys Thr Val Thr Thr Val Glu Thr Gln Asn
35 40 45

Leu Glu Gly Leu His His Asp Gly Gln Phe Cys His Lys Pro Cys Pro
50 55 60

Pro Gly Glu Arg Lys Ala Arg Asp Cys Thr Val Asn Gly Asp Glu Pro
65 70 75 80

Asp Cys Val Pro Cys Gln Glu Gly Lys Glu Tyr Thr Asp Lys Ala His
85 90 95

Phe Ser Ser Lys Cys Arg Arg Cys Arg Leu Cys Asp Glu Gly His Gly
100 105 110

Leu Glu Val Glu Ile Asn Cys Thr Arg Thr Gln Asn Thr Lys Cys Arg
115 120 125

Cys Lys Pro Asn Phe Phe Cys Asn Ser Thr Val Cys Glu His Cys Asp
130 135 140

Pro Cys Thr Lys Cys Glu His Gly Ile Ile Lys Glu Cys Thr Leu Thr
145 150 155 160

Ser Asn Thr Lys Cys Lys Glu Glu Gly Ser Arg Ser Asn Leu Gly Trp
165 170 175

Leu Cys Leu Leu Leu Leu Pro Ile Pro Leu Ile Val Trp Val Lys Arg
180 185 190

Lys Glu Val Gln Lys Thr Cys Arg Lys His Arg Lys Glu Asn Gln Gly
195 200 205

Ser His Glu Ser Pro Thr Leu Asn Pro Glu Thr Val Ala Ile Asn Leu
210 215 220

Ser Asp Val Asp Leu Ser Lys Tyr Ile Thr Thr Ile Ala Gly Val Met

225	230	235	240
Thr Leu Ser Gln Val Lys Gly Phe Val Arg Lys Asn Gly Val Asn Glu			
245	250	255	
Ala Lys Ile Asp Glu Ile Lys Asn Asp Asn Val Gln Asp Thr Ala Glu			
260	265	270	
Gln Lys Val Gln Leu Leu Arg Asn Trp His Gln Leu His Gly Lys Lys			
275	280	285	
Glu Ala Tyr Asp Thr Leu Ile Lys Asp Leu Lys Lys Ala Asn Leu Cys			
290	295	300	
Thr Leu Ala Glu Lys Ile Gln Thr Ile Ile Leu Lys Asp Ile Thr Ser			
305	310	315	320
Asp Ser Glu Asn Ser Asn Phe Arg Asn Glu Ile Gln Ser Leu Val			
325	330	335	

<210> 13
 <211> 1642
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (130)..(756)

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 gaccccgcc atg gac ccg ttc ctg gtg ctg ctg cac tcg gtg tgc tcc agc 171
 Met Asp Pro Phe Leu Val Leu Leu His Ser Val Ser Ser Ser
 1 5 10

ctg tgc agc agc gag ctg acc gag ctc aag ttc cta tgc ctc ggg cgc 219
 Leu Ser Ser Ser Glu Leu Thr Glu Leu Lys Phe Leu Cys Leu Gly Arg
 15 20 25 30

gtg ggc aag cgc aag ctg gag cgc gtg cag agc ggc cta gac ctc ttc 267
 Val Gly Lys Arg Lys Leu Glu Arg Val Gln Ser Gly Leu Asp Leu Phe
 35 40 45

tcc atg ctg ctg gag cag aac gac ctg gag ccc ggg cac acc gag ctc 315

Ser Met Leu Leu Glu Gln Asn Asp Leu Glu Pro Gly His Thr Glu Leu
 50 55 60

ctg cgc gag ctg ctc gcc tcc ctg cgg cgc cac gac ctg ctg cgg cgc 363
 Leu Arg Glu Leu Leu Ala Ser Leu Arg Arg His Asp Leu Leu Arg Arg
 65 70 75

gtc gac gac ttc gag gcg ggg gcg gcg gcc ggg gcc gcg cct ggg gaa 411
 Val Asp Asp Phe Glu Ala Gly Ala Ala Ala Gly Ala Ala Pro Gly Glu
 80 85 90

gaa gac ctg tgt gca gca ttt aac gtc ata tgt gat aat gtg ggg aaa 459
 Glu Asp Leu Cys Ala Ala Phe Asn Val Ile Cys Asp Asn Val Gly Lys
 95 100 105 110

gat tgg aga agg ctg gct cgt cag ctc aaa gtc tca gac acc aag atc 507
 Asp Trp Arg Arg Leu Ala Arg Gln Leu Lys Val Ser Asp Thr Lys Ile
 115 120 125

gac agc atc gag gac aga tac ccc cgc aac ctg aca gag cgt gtg cgg 555
 Asp Ser Ile Glu Asp Arg Tyr Pro Arg Asn Leu Thr Glu Arg Val Arg
 130 135 140

gag tca ctg aga atc tgg aag aac aca gag aag gag aac gca aca gtg 603
 Glu Ser Leu Arg Ile Trp Lys Asn Thr Glu Lys Glu Asn Ala Thr Val
 145 150 155

gcc cac ctg gtg ggg gct ctc agg tcc tgc cag atg aac ctg gtg gct 651
 Ala His Leu Val Gly Ala Leu Arg Ser Cys Gln Met Asn Leu Val Ala
 160 165 170

gac ctg gta caa gag gtt cag cag gcc cgt gac ctc cag aac agg agt 699
 Asp Leu Val Gln Glu Val Gln Gln Ala Arg Asp Leu Gln Asn Arg Ser
 175 180 185 190

ggg gcc atg tcc ccg atg tca tgg aac tca gac gca tct acc tcc gaa 747
 Gly Ala Met Ser Pro Met Ser Trp Asn Ser Asp Ala Ser Thr Ser Glu
 195 200 205

gcg tcc tga tgggcccgtg ctttgcgctg gtggaccaca ggcattctaca 796
 Ala Ser

cagcctggac tttggttctc tccaggaagg tagcccagca ctgtgaagac ccagcaggaa 856

gccaggctga gtgagccaca gaccacctgc ttctgaactc aagctgcgtt tattaatgcc 916

tctcccgcac caggccgggc ttgggcccctg cacagatatt tccatttctt cctcactatg 976

aactgagca agatcttgtc tccactaaat gagctcctgc gggagtagtt ggaaagttgg 1036
 aaccgtgtcc agcacagaag gaatctgtgc agatgagcag tcacactgtt actccacagc 1096
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 caattctaca gtttcttact gttttgtatc aaaatcacta tctttctgat aacagaattg 1576
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 ttaaaa 1642

<210> 14

<211> 208

<212> PRT

<213> Homo sapiens

<400> 14

Met	Asp	Pro	Phe	Leu	Val	Leu	Leu	His	Ser	Val	Ser	Ser	Ser	Leu	Ser
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Ser	Ser	Glu	Leu	Thr	Glu	Leu	Lys	Phe	Leu	Cys	Leu	Gly	Arg	Val	Gly
			20					25					30		
Lys	Arg	Lys	Leu	Glu	Arg	Val	Gln	Ser	Gly	Leu	Asp	Leu	Phe	Ser	Met
		35					40					45			
Leu	Leu	Glu	Gln	Asn	Asp	Leu	Glu	Pro	Gly	His	Thr	Glu	Leu	Leu	Arg
	50					55				60					
Glu	Leu	Leu	Ala	Ser	Leu	Arg	Arg	His	Asp	Leu	Leu	Arg	Arg	Val	Asp
65					70				75					80	
Asp	Phe	Glu	Ala	Gly	Ala	Ala	Ala	Gly	Ala	Ala	Pro	Gly	Glu	Glu	Asp
			85					90						95	

Leu Cys Ala Ala Phe Asn Val Ile Cys Asp Asn Val Gly Lys Asp Trp
 100 105 110
 Arg Arg Leu Ala Arg Gln Leu Lys Val Ser Asp Thr Lys Ile Asp Ser
 115 120 125
 Ile Glu Asp Arg Tyr Pro Arg Asn Leu Thr Glu Arg Val Arg Glu Ser
 130 135 140
 Leu Arg Ile Trp Lys Asn Thr Glu Lys Glu Asn Ala Thr Val Ala His
 145 150 155 160
 Leu Val Gly Ala Leu Arg Ser Cys Gln Met Asn Leu Val Ala Asp Leu
 165 170 175
 Val Gln Glu Val Gln Gln Ala Arg Asp Leu Gln Asn Arg Ser Gly Ala
 180 185 190
 Met Ser Pro Met Ser Trp Asn Ser Asp Ala Ser Thr Ser Glu Ala Ser
 195 200 205

<210> 15
 <211> 1883
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (257)..(1747)

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 agaaggtgac tgggtggctgc ctgaggaata ccagtgggca agagaattag catttctgga 120
 gcatctgctg tctgagcagc cctgggtgac gtccactttc tgggcacgtg aggttgggac 180
 ttggccgcct gagcccttga gttgggtcact tgaaccttgg gaatattgag attatattct 240
 cctgcctttt aaaaag atg gac ttc agc aga aat ctt tat gat att ggg gaa 292
 Met Asp Phe Ser Arg Asn Leu Tyr Asp Ile Gly Glu
 1 5 10
 caa ctg gac agt gaa gat ctg gcc tcc ctc aag ttc ctg agc ctg gac 340
 Gln Leu Asp Ser Glu Asp Leu Ala Ser Leu Lys Phe Leu Ser Leu Asp
 15 20 25

tac att ccg caa agg aag caa gaa ccc atc aag gat gcc ttg atg tta	388
Tyr Ile Pro Gln Arg Lys Gln Glu Pro Ile Lys Asp Ala Leu Met Leu	
30 35 40	
ttc cag aga ctc cag gaa aag aga atg ttg gag gaa agc aat ctg tcc	436
Phe Gln Arg Leu Gln Glu Lys Arg Met Leu Glu Glu Ser Asn Leu Ser	
45 50 55 60	
ttc ctg aag gag ctg ctc ttc cga att aat aga ctg gat ttg ctg att	484
Phe Leu Lys Glu Leu Leu Phe Arg Ile Asn Arg Leu Asp Leu Leu Ile	
65 70 75	
acc tac cta aac act aga aag gag gag atg gaa agg gaa ctt cag aca	532
Thr Tyr Leu Asn Thr Arg Lys Glu Glu Met Glu Arg Glu Leu Gln Thr	
80 85 90	
cca ggc agg gct caa att tct gcc tac agg ttc cac ttc tgc cgc atg	580
Pro Gly Arg Ala Gln Ile Ser Ala Tyr Arg Phe His Phe Cys Arg Met	
95 100 105	
agc tgg gct gaa gca aac agc cag tgc cag aca cag tct gta cct ttc	628
Ser Trp Ala Glu Ala Asn Ser Gln Cys Gln Thr Gln Ser Val Pro Phe	
110 115 120	
tgg cgg agg gtc gat cat cta tta ata agg gtc atg ctc tat cag att	676
Trp Arg Arg Val Asp His Leu Leu Ile Arg Val Met Leu Tyr Gln Ile	
125 130 135 140	
tca gaa gaa gtg agc aga tca gaa ttg agg tct ttt aag ttt ctt ttg	724
Ser Glu Glu Val Ser Arg Ser Glu Leu Arg Ser Phe Lys Phe Leu Leu	
145 150 155	
caa gag gaa atc tcc aaa tgc aaa ctg gat gat gac atg aac ctg ctg	772
Gln Glu Glu Ile Ser Lys Cys Lys Leu Asp Asp Asp Met Asn Leu Leu	
160 165 170	
gat att ttc ata gag atg gag aag agg gtc atc ctg gga gaa gga aag	820
Asp Ile Phe Ile Glu Met Glu Lys Arg Val Ile Leu Gly Glu Gly Lys	
175 180 185	
ttg gac atc ctg aaa aga gtc tgt gcc caa atc aac aag agc ctg ctg	868
Leu Asp Ile Leu Lys Arg Val Cys Ala Gln Ile Asn Lys Ser Leu Leu	
190 195 200	
aag ata atc aac gac tat gaa gaa ttc agc aaa ggg gag gag ttg tgt	916
Lys Ile Ile Asn Asp Tyr Glu Glu Phe Ser Lys Gly Glu Glu Leu Cys	
205 210 215 220	

ggg gta atg aca atc tcg gac tct cca aga gaa cag gat agt gaa tca	964
Gly Val Met Thr Ile Ser Asp Ser Pro Arg Glu Gln Asp Ser Glu Ser	
225 230 235	
cag act ttg gac aaa gtt tac caa atg aaa agc aaa cct cgg gga tac	1012
Gln Thr Leu Asp Lys Val Tyr Gln Met Lys Ser Lys Pro Arg Gly Tyr	
240 245 250	
tgt ctg atc atc aac aat cac aat ttt gca aaa gca cgg gag aaa gtg	1060
Cys Leu Ile Ile Asn Asn His Asn Phe Ala Lys Ala Arg Glu Lys Val	
255 260 265	
ccc aaa ctt cac agc att agg gac agg aat gga aca cac ttg gat gca	1108
Pro Lys Leu His Ser Ile Arg Asp Arg Asn Gly Thr His Leu Asp Ala	
270 275 280	
ggg gct ttg acc acg acc ttt gaa gag ctt cat ttt gag atc aag ccc	1156
Gly Ala Leu Thr Thr Thr Phe Glu Glu Leu His Phe Glu Ile Lys Pro	
285 290 295 300	
cac cat gac tgc aca gta gag caa atc tat gag att ttg aaa atc tac	1204
His His Asp Cys Thr Val Glu Gln Ile Tyr Glu Ile Leu Lys Ile Tyr	
305 310 315	
caa ctc atg gac cac agt aac atg gac tgc ttc atc tgc tgt atc ctc	1252
Gln Leu Met Asp His Ser Asn Met Asp Cys Phe Ile Cys Cys Ile Leu	
320 325 330	
tcc cat gga gac aag ggc atc atc tat ggc act gat gga cag gag gcc	1300
Ser His Gly Asp Lys Gly Ile Ile Tyr Gly Thr Asp Gly Gln Glu Ala	
335 340 345	
ccc atc tat gag ctg aca tct cag ttc act ggt ttg aag tgc cct tcc	1348
Pro Ile Tyr Glu Leu Thr Ser Gln Phe Thr Gly Leu Lys Cys Pro Ser	
350 355 360	
ctt gct gga aaa ccc aaa gtg ttt ttt att cag gct tgt cag ggg gat	1396
Leu Ala Gly Lys Pro Lys Val Phe Phe Ile Gln Ala Cys Gln Gly Asp	
365 370 375 380	
aac tac cag aaa ggt ata cct gtt gag act gat tca gag gag caa ccc	1444
Asn Tyr Gln Lys Gly Ile Pro Val Glu Thr Asp Ser Glu Glu Gln Pro	
385 390 395	
tat tta gaa atg gat tta tca tca cct caa acg aga tat atc ccg gat	1492
Tyr Leu Glu Met Asp Leu Ser Ser Pro Gln Thr Arg Tyr Ile Pro Asp	
400 405 410	

gag gct gac ttt ctg ctg ggg atg gcc act gtg aat aac tgt gtt tcc 1540
 Glu Ala Asp Phe Leu Leu Gly Met Ala Thr Val Asn Asn Cys Val Ser
 415 420 425

tac cga aac cct gca gag gga acc tgg tac atc cag tca ctt tgc cag 1588
 Tyr Arg Asn Pro Ala Glu Gly Thr Trp Tyr Ile Gln Ser Leu Cys Gln
 430 435 440

agc ctg aga gag cga tgt cct cga ggc gat gat att ctc acc atc ctg 1636
 Ser Leu Arg Glu Arg Cys Pro Arg Gly Asp Asp Ile Leu Thr Ile Leu
 445 450 455 460

act gaa gtg aac tat gaa gta agc aac aag gat gac aag aaa aac atg 1684
 Thr Glu Val Asn Tyr Glu Val Ser Asn Lys Asp Asp Lys Lys Asn Met
 465 470 475

ggg aaa cag atg cct cag cct act ttc aca cta aga aaa aaa ctt gtc 1732
 Gly Lys Gln Met Pro Gln Pro Thr Phe Thr Leu Arg Lys Lys Leu Val
 480 485 490

ttc cct tct gat tga tgggtgctatt ttgtttgttt tggtttgttt tggttttttg 1787
 Phe Pro Ser Asp
 495

agacagaatc tcgctctgtc gcccgaggctg gaggcagtg gcgtgatctc ggctcaccgc 1847

aagctccgcc tcccgggttc aggccattct cctgct 1883

<210> 16

<211> 496

<212> PRT

<213> Homo sapiens

<400> 16

Met Asp Phe Ser Arg Asn Leu Tyr Asp Ile Gly Glu Gln Leu Asp Ser
 1 5 10 15

Glu Asp Leu Ala Ser Leu Lys Phe Leu Ser Leu Asp Tyr Ile Pro Gln
 20 25 30

Arg Lys Gln Glu Pro Ile Lys Asp Ala Leu Met Leu Phe Gln Arg Leu
 35 40 45

Gln Glu Lys Arg Met Leu Glu Glu Ser Asn Leu Ser Phe Leu Lys Glu
 50 55 60

Leu Leu Phe Arg Ile Asn Arg Leu Asp Leu Leu Ile Thr Tyr Leu Asn
 65 70 75 80

Thr Arg Lys Glu Glu Met Glu Arg Glu Leu Gln Thr Pro Gly Arg Ala
 85 90 95

Gln Ile Ser Ala Tyr Arg Phe His Phe Cys Arg Met Ser Trp Ala Glu
 100 105 110

Ala Asn Ser Gln Cys Gln Thr Gln Ser Val Pro Phe Trp Arg Arg Val
 115 120 125

Asp His Leu Leu Ile Arg Val Met Leu Tyr Gln Ile Ser Glu Glu Val
 130 135 140

Ser Arg Ser Glu Leu Arg Ser Phe Lys Phe Leu Leu Gln Glu Glu Ile
 145 150 155 160

Ser Lys Cys Lys Leu Asp Asp Asp Met Asn Leu Leu Asp Ile Phe Ile
 165 170 175

Glu Met Glu Lys Arg Val Ile Leu Gly Glu Gly Lys Leu Asp Ile Leu
 180 185 190

Lys Arg Val Cys Ala Gln Ile Asn Lys Ser Leu Leu Lys Ile Ile Asn
 195 200 205

Asp Tyr Glu Glu Phe Ser Lys Gly Glu Glu Leu Cys Gly Val Met Thr
 210 215 220

Ile Ser Asp Ser Pro Arg Glu Gln Asp Ser Glu Ser Gln Thr Leu Asp
 225 230 235 240

Lys Val Tyr Gln Met Lys Ser Lys Pro Arg Gly Tyr Cys Leu Ile Ile
 245 250 255

Asn Asn His Asn Phe Ala Lys Ala Arg Glu Lys Val Pro Lys Leu His
 260 265 270

Ser Ile Arg Asp Arg Asn Gly Thr His Leu Asp Ala Gly Ala Leu Thr
 275 280 285

Thr Thr Phe Glu Glu Leu His Phe Glu Ile Lys Pro His His Asp Cys
 290 295 300

Thr Val Glu Gln Ile Tyr Glu Ile Leu Lys Ile Tyr Gln Leu Met Asp
 305 310 315 320

His Ser Asn Met Asp Cys Phe Ile Cys Cys Ile Leu Ser His Gly Asp
325 330 335

Lys Gly Ile Ile Tyr Gly Thr Asp Gly Gln Glu Ala Pro Ile Tyr Glu
340 345 350

Leu Thr Ser Gln Phe Thr Gly Leu Lys Cys Pro Ser Leu Ala Gly Lys
355 360 365

Pro Lys Val Phe Phe Ile Gln Ala Cys Gln Gly Asp Asn Tyr Gln Lys
370 375 380

Gly Ile Pro Val Glu Thr Asp Ser Glu Glu Gln Pro Tyr Leu Glu Met
385 390 395 400

Asp Leu Ser Ser Pro Gln Thr Arg Tyr Ile Pro Asp Glu Ala Asp Phe
405 410 415

Leu Leu Gly Met Ala Thr Val Asn Asn Cys Val Ser Tyr Arg Asn Pro
420 425 430

Ala Glu Gly Thr Trp Tyr Ile Gln Ser Leu Cys Gln Ser Leu Arg Glu
435 440 445

Arg Cys Pro Arg Gly Asp Asp Ile Leu Thr Ile Leu Thr Glu Val Asn
450 455 460

Tyr Glu Val Ser Asn Lys Asp Asp Lys Lys Asn Met Gly Lys Gln Met
465 470 475 480

Pro Gln Pro Thr Phe Thr Leu Arg Lys Lys Leu Val Phe Pro Ser Asp
485 490 495

<210> 17

<211> 702

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(702)

<400> 17

atg agc act gaa agc atg atc cgg gac gtg gag ctg gcc gag gag gcg 48

Met Ser Thr Glu Ser Met Ile Arg Asp Val Glu Leu Ala Glu Glu Ala

1

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10

15

ctc ccc aag aag aca ggg ggg ccc cag ggc tcc agg cgg tgc ttg ttc	96
Leu Pro Lys Lys Thr Gly Gly Pro Gln Gly Ser Arg Arg Cys Leu Phe	
20 25 30	
ctc agc ctc ttc tcc ttc ctg atc gtg gca ggc gcc acc acg ctc ttc	144
Leu Ser Leu Phe Ser Phe Leu Ile Val Ala Gly Ala Thr Thr Leu Phe	
35 40 45	
tgc ctg ctg cac ttt gga gtg atc ggc ccc cag agg gaa gag ttc ccc	192
Cys Leu Leu His Phe Gly Val Ile Gly Pro Gln Arg Glu Glu Phe Pro	
50 55 60	
agg gac ctc tct cta atc agc cct ctg gcc cag gca gtc aga tca tct	240
Arg Asp Leu Ser Leu Ile Ser Pro Leu Ala Gln Ala Val Arg Ser Ser	
65 70 75 80	
tct cga acc ccg agt gac aag cct gta gcc cat gtt gta gca aac cct	288
Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His Val Val Ala Asn Pro	
85 90 95	
caa gct gag ggg cag ctc cag tgg ctg aac cgc cgg gcc aat gcc ctc	336
Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu	
100 105 110	
ctg gcc aat ggc gtg gag ctg aga gat aac cag ctg gtg gtg cca tca	384
Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser	
115 120 125	
gag ggc ctg tac ctc atc tac tcc cag gtc ctc ttc aag ggc caa ggc	432
Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly	
130 135 140	
tgc ccc tcc acc cat gtg ctc ctc acc cac acc atc agc cgc atc gcc	480
Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala	
145 150 155 160	
gtc tcc tac cag acc aag gtc aac ctc ctc tct gcc atc aag agc ccc	528
Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro	
165 170 175	
tgc cag agg gag acc cca gag ggg gct gag gcc aag ccc tgg tat gag	576
Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu	
180 185 190	
ccc atc tat ctg gga ggg gtc ttc cag ctg gag aag ggt gac cga ctc	624
Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu	
195 200 205	

agc gct gag atc aat cgg ccc gac tat ctg gac ttt gcc gag tct ggg 672
 Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly
 210 215 220

cag gtc tac ttt ggg atc att gcc ctg tga 702
 Gln Val Tyr Phe Gly Ile Ile Ala Leu
 225 230

<210> 18
 <211> 233
 <212> PRT
 <213> Homo sapiens

<400> 18
 Met Ser Thr Glu Ser Met Ile Arg Asp Val Glu Leu Ala Glu Glu Ala
 1 5 10 15

Leu Pro Lys Lys Thr Gly Gly Pro Gln Gly Ser Arg Arg Cys Leu Phe
 20 25 30

Leu Ser Leu Phe Ser Phe Leu Ile Val Ala Gly Ala Thr Thr Leu Phe
 35 40 45

Cys Leu Leu His Phe Gly Val Ile Gly Pro Gln Arg Glu Glu Phe Pro
 50 55 60

Arg Asp Leu Ser Leu Ile Ser Pro Leu Ala Gln Ala Val Arg Ser Ser
 65 70 75 80

Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His Val Val Ala Asn Pro
 85 90 95

Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu
 100 105 110

Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser
 115 120 125

Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly
 130 135 140

Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala
 145 150 155 160

Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro
 165 170 175

Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu
 180 185 190

Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu
 195 200 205

Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly
 210 215 220

Gln Val Tyr Phe Gly Ile Ile Ala Leu
 225 230

<210> 19

<211> 1306

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (18)..(767)

<400> 19

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Met Ala Ala Arg Arg Ser Gln Arg Arg Arg Gly
 1 5 10

cgc cgg ggg gag ccg ggc acc gcc ctg ctg gtc ccg ctc gcg ctg ggc 98

Arg Arg Gly Glu Pro Gly Thr Ala Leu Leu Val Pro Leu Ala Leu Gly
 15 20 25

ctg ggc ctg gcg ctg gcc tgc ctc ggc ctc ctg ctg gcc gtg gtc agt 146

Leu Gly Leu Ala Leu Ala Cys Leu Gly Leu Leu Leu Ala Val Val Ser
 30 35 40

ttg ggg agc cgg gca tcg ctg tcc gcc cag gag cct gcc cag gag gag 194

Leu Gly Ser Arg Ala Ser Leu Ser Ala Gln Glu Pro Ala Gln Glu Glu
 45 50 55

ctg gtg gca gag gag gac cag gac ccg tcg gaa ctg aat ccc cag aca 242

Leu Val Ala Glu Glu Asp Gln Asp Pro Ser Glu Leu Asn Pro Gln Thr
 60 65 70 75

gaa gaa agc cag gat cct gcg cct ttc ctg aac cga cta gtt cgg cct 290

Glu Glu Ser Gln Asp Pro Ala Pro Phe Leu Asn Arg Leu Val Arg Pro
 80 85 90

cgc aga agt gca cct aaa ggc cgg aaa aca cgg gct cga aga gcg atc 338

Arg Arg Ser Ala Pro Lys Gly Arg Lys Thr Arg Ala Arg Arg Ala Ile	
95 100 105	
gca gcc cat tat gaa gtt cat cca cga cct gga cag gac gga gcg cag	386
Ala Ala His Tyr Glu Val His Pro Arg Pro Gly Gln Asp Gly Ala Gln	
110 115 120	
gca ggt gtg gac ggg aca gtg agt ggc tgg gag gaa gcc aga atc aac	434
Ala Gly Val Asp Gly Thr Val Ser Gly Trp Glu Glu Ala Arg Ile Asn	
125 130 135	
agc tcc agc cct ctg cgc tac aac cgc cag atc ggg gag ttt ata gtc	482
Ser Ser Ser Pro Leu Arg Tyr Asn Arg Gln Ile Gly Glu Phe Ile Val	
140 145 150 155	
acc cgg gct ggg ctc tac tac ctg tac tgt cag gtg cac ttt gat gag	530
Thr Arg Ala Gly Leu Tyr Tyr Leu Tyr Cys Gln Val His Phe Asp Glu	
160 165 170	
ggg aag gct gtc tac ctg aag ctg gac ttg ctg gtg gat ggt gtg ctg	578
Gly Lys Ala Val Tyr Leu Lys Leu Asp Leu Leu Val Asp Gly Val Leu	
175 180 185	
gcc ctg cgc tgc ctg gag gaa ttc tca gcc act gcg gcc agt tcc ctc	626
Ala Leu Arg Cys Leu Glu Glu Phe Ser Ala Thr Ala Ala Ser Ser Leu	
190 195 200	
ggg ccc cag ctc cgc ctc tgc cag gtg tct ggg ctg ttg gcc ctg cgg	674
Gly Pro Gln Leu Arg Leu Cys Gln Val Ser Gly Leu Leu Ala Leu Arg	
205 210 215	
cca ggg tcc tcc ctg cgg atc cgc acc ctc ccc tgg gcc cat ctc aag	722
Pro Gly Ser Ser Leu Arg Ile Arg Thr Leu Pro Trp Ala His Leu Lys	
220 225 230 235	
gct gcc ccc ttc ctc acc tac ttc gga ctc ttc cag gtt cac tga	767
Ala Ala Pro Phe Leu Thr Tyr Phe Gly Leu Phe Gln Val His	
240 245 250	
ggggccctgg tctccccaca gtcgtccag gctgccggt cccctcgaca gctctctggg	827
caccgggtcc cctctgcccc accctcagcc gctctttgct ccagacctgc cctccctct	887
agaggctgcc tgggcctgtt cacgtgtttt ccatccaca taaatacagt attcccactc	947
ttatcttaca actccccac cgcccactct ccacctcact agtccccaa tccctgacct	1007
tttgaggccc ccagtgatct cgactcccc ctggccacag acccccaggg cattgtgttc	1067

actgtactct gtgggcaagg atgggtccag aagacccac ttcaggcact aagaggggct 1127
 ggacctggcg gcaggaagcc aaagagactg ggcctaggcc aggagttccc aaatgtgagg 1187
 ggcgagaaac aagacaagct cctcccttga gaattccctg tggattttta aaacagatat 1247
 tatttttatt attattgtga caaatgttg ataatggat attaataga ataagtcag 1306

<210> 20
 <211> 249
 <212> PRT
 <213> Homo sapiens

<400> 20

Met Ala Ala Arg Arg Ser Gln Arg Arg Arg Gly Arg Arg Gly Glu Pro
 1 5 10 15

Gly Thr Ala Leu Leu Val Pro Leu Ala Leu Gly Leu Gly Leu Ala Leu
 20 25 30

Ala Cys Leu Gly Leu Leu Leu Ala Val Val Ser Leu Gly Ser Arg Ala
 35 40 45

Ser Leu Ser Ala Gln Glu Pro Ala Gln Glu Glu Leu Val Ala Glu Glu
 50 55 60

Asp Gln Asp Pro Ser Glu Leu Asn Pro Gln Thr Glu Glu Ser Gln Asp
 65 70 75 80

Pro Ala Pro Phe Leu Asn Arg Leu Val Arg Pro Arg Arg Ser Ala Pro
 85 90 95

Lys Gly Arg Lys Thr Arg Ala Arg Arg Ala Ile Ala Ala His Tyr Glu
 100 105 110

Val His Pro Arg Pro Gly Gln Asp Gly Ala Gln Ala Gly Val Asp Gly
 115 120 125

Thr Val Ser Gly Trp Glu Glu Ala Arg Ile Asn Ser Ser Ser Pro Leu
 130 135 140

Arg Tyr Asn Arg Gln Ile Gly Glu Phe Ile Val Thr Arg Ala Gly Leu
 145 150 155 160

Tyr Tyr Leu Tyr Cys Gln Val His Phe Asp Glu Gly Lys Ala Val Tyr
 165 170 175

Leu Lys Leu Asp Leu Leu Val Asp Gly Val Leu Ala Leu Arg Cys Leu
 180 185 190

Glu Glu Phe Ser Ala Thr Ala Ala Ser Ser Leu Gly Pro Gln Leu Arg
 195 200 205

Leu Cys Gln Val Ser Gly Leu Leu Ala Leu Arg Pro Gly Ser Ser Leu
 210 215 220

Arg Ile Arg Thr Leu Pro Trp Ala His Leu Lys Ala Ala Pro Phe Leu
 225 230 235 240

Thr Tyr Phe Gly Leu Phe Gln Val His
 245

<210> 21

<211> 1769

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (88)..(933)

<400> 21

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ttacagcagt cagactctga caggatc atg gct atg atg gag gtc cag ggg gga 114
 Met Ala Met Met Glu Val Gln Gly Gly

1

5

ccc agc ctg gga cag acc tgc gtg ctg atc gtg atc ttc aca gtg ctc 162
 Pro Ser Leu Gly Gln Thr Cys Val Leu Ile Val Ile Phe Thr Val Leu
 10 15 20 25

ctg cag tct ctc tgt gtg gct gta act tac gtg tac ttt acc aac gag 210
 Leu Gln Ser Leu Cys Val Ala Val Thr Tyr Val Tyr Phe Thr Asn Glu
 30 35 40

ctg aag cag atg cag gac aag tac tcc aaa agt ggc att gct tgt ttc 258
 Leu Lys Gln Met Gln Asp Lys Tyr Ser Lys Ser Gly Ile Ala Cys Phe
 45 50 55

tta aaa gaa gat gac agt tat tgg gac ccc aat gac gaa gag agt atg 306
 Leu Lys Glu Asp Asp Ser Tyr Trp Asp Pro Asn Asp Glu Glu Ser Met
 60 65 70

aac agc ccc tgc tgg caa gtc aag tgg caa ctc cgt cag ctc gtt aga	354
Asn Ser Pro Cys Trp Gln Val Lys Trp Gln Leu Arg Gln Leu Val Arg	
75 80 85	
aag atg att ttg aga acc tct gag gaa acc att tct aca gtt caa gaa	402
Lys Met Ile Leu Arg Thr Ser Glu Glu Thr Ile Ser Thr Val Gln Glu	
90 95 100 105	
aag caa caa aat att tct ccc cta gtg aga gaa aga ggt cct cag aga	450
Lys Gln Gln Asn Ile Ser Pro Leu Val Arg Glu Arg Gly Pro Gln Arg	
110 115 120	
gta gca gct cac ata act ggg acc aga gga aga agc aac aca ttg tct	498
Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser	
125 130 135	
tct cca aac tcc aag aat gaa aag gct ctg ggc cgc aaa ata aac tcc	546
Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser	
140 145 150	
tgg gaa tca tca agg agt ggg cat tca ttc ctg agc aac ttg cac ttg	594
Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His Leu	
155 160 165	
agg aat ggt gaa ctg gtc atc cat gaa aaa ggg ttt tac tac atc tat	642
Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr	
170 175 180 185	
tcc caa aca tac ttt cga ttt cag gag gaa ata aaa gaa aac aca aag	690
Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys	
190 195 200	
aac gac aaa caa atg gtc caa tat att tac aaa tac aca agt tat cct	738
Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro	
205 210 215	
gac cct ata ttg ttg atg aaa agt gct aga aat agt tgt tgg tct aaa	786
Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys	
220 225 230	
gat gca gaa tat gga ctc tat tcc atc tat caa ggg gga ata ttt gag	834
Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu	
235 240 245	
ctt aag gaa aat gac aga att ttt gtt tct gta aca aat gag cac ttg	882
Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His Leu	
250 255 260 265	

ata gac atg gac cat gaa gcc agt ttt ttc ggg gcc ttt tta gtt ggc 930
 Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val Gly
 270 275 280

taa ctgacctgga aagaaaaagc aataacctca aagtgactat tcagttttca 983

ggatgatata ctatgaagat gtttcaaaaa atctgaccaa aacaaacaaa cagaaaacag 1043

aaaacaaaaa aacctctatg caatctgagt agagcagcca caaccaaaaa attctacaac 1103

acacactgtt ctgaaagtga ctcaattatc ccaagaaaat gaaattgctg aaagatcttt 1163

caggactcta cctcatatca gtttgctagc agaaatctag aagactgtca gtttccaaac 1223

attaatgcaa tggttaacat cttctgtctt tataatctac tccttgtaaa gactgtagaa 1283

gaaagcgcaa caatccatct ctcaagtagt gtatcacagt agtagcctcc aggtttcctt 1343

aagggacaac atccttaagt caaaagagag aagaggcacc actaaaagat cgcagtttgc 1403

ctggtgcagt ggctcacacc tgtaatccca acattttggg aaccaaggt gggtagatca 1463

cgagatcaag agatcaagac catagtgacc aacatagtga aaccccatct ctactgaaag 1523

tgcaaaaatt agctgggtgt gttggcacat gcctgtagtc ccagctactt gagaggctga 1583

ggcaggagaa tcgtttgaac ccgggaggca gaggttgagc tgtggtgaga tcatgccact 1643

acactccagc ctggcgacag agcgagactt ggtttcaaaa aaaaaaaaaa aaaaaaactt 1703

cagtaagtac gtgttatattt tttcaataaa attctattac agtatgtcaa aaaaaaaaaa 1763

aaaaaa 1769

<210> 22

<211> 281

<212> PRT

<213> Homo sapiens

<400> 22

Met Ala Met Met Glu Val Gln Gly Gly Pro Ser Leu Gly Gln Thr Cys

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5

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15

Val Leu Ile Val Ile Phe Thr Val Leu Leu Gln Ser Leu Cys Val Ala

20

25

30

Val Thr Tyr Val Tyr Phe Thr Asn Glu Leu Lys Gln Met Gln Asp Lys
35 40 45
Tyr Ser Lys Ser Gly Ile Ala Cys Phe Leu Lys Glu Asp Asp Ser Tyr
50 55 60
Trp Asp Pro Asn Asp Glu Glu Ser Met Asn Ser Pro Cys Trp Gln Val
65 70 75 80
Lys Trp Gln Leu Arg Gln Leu Val Arg Lys Met Ile Leu Arg Thr Ser
85 90 95
Glu Glu Thr Ile Ser Thr Val Gln Glu Lys Gln Gln Asn Ile Ser Pro
100 105 110
Leu Val Arg Glu Arg Gly Pro Gln Arg Val Ala Ala His Ile Thr Gly
115 120 125
Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu
130 135 140
Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly
145 150 155 160
His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val Ile
165 170 175
His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe
180 185 190
Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val Gln
195 200 205
Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys
210 215 220
Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr
225 230 235 240
Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile
245 250 255
Phe Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu Ala
260 265 270
Ser Phe Phe Gly Ala Phe Leu Val Gly
275 280

<210> 23
 <211> 1042
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (91)..(936)

<400> 23

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gacttacagc agtcagactc tgacaggatc atg gct atg atg gag gtc cag ggg 114
 Met Ala Met Met Glu Val Gln Gly
 1 5

gga ccc agc ctg gga cag acc tgc gtg ctg atc gtg atc ttc aca gtg 162
 Gly Pro Ser Leu Gly Gln Thr Cys Val Leu Ile Val Ile Phe Thr Val
 10 15 20

ctc ctg cag tct ctc tgt gtg gct gta act tac gtg tac ttt acc aac 210
 Leu Leu Gln Ser Leu Cys Val Ala Val Thr Tyr Val Tyr Phe Thr Asn
 25 30 35 40

gag ctg aag cag atg cag gac aag tac tcc aaa agt ggc att gct tgt 258
 Glu Leu Lys Gln Met Gln Asp Lys Tyr Ser Lys Ser Gly Ile Ala Cys
 45 50 55

ttc tta aaa gaa gat gac agt tat tgg gac ccc aat gac gaa gag agt 306
 Phe Leu Lys Glu Asp Asp Ser Tyr Trp Asp Pro Asn Asp Glu Glu Ser
 60 65 70

atg aac agc ccc tgc tgg caa gtc aag tgg caa ctc cgt cag ctc gtt 354
 Met Asn Ser Pro Cys Trp Gln Val Lys Trp Gln Leu Arg Gln Leu Val
 75 80 85

aga aag atg att ttg aga acc tct gag gaa acc att tct aca gtt caa 402
 Arg Lys Met Ile Leu Arg Thr Ser Glu Glu Thr Ile Ser Thr Val Gln
 90 95 100

gaa aag caa caa aat att tct ccc cta gtg aga gaa aga ggt cct cag 450
 Glu Lys Gln Gln Asn Ile Ser Pro Leu Val Arg Glu Arg Gly Pro Gln
 105 110 115 120

aga gta gca gct cac ata act ggg acc aga gga aga agc aac aca ttg 498
 Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu

125	130	135	
tct tct cca aac tcc aag aat gaa aag gct ctg ggc cgc aaa ata aac			546
Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn			
140	145	150	
tcc tgg gaa tca tca agg agt ggg cat tca ttc ctg agc aac ttg cac			594
Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His			
155	160	165	
ttg agg aat ggt gaa ctg gtc atc cat gaa aaa ggg ttt tac tac atc			642
Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile			
170	175	180	
tat tcc caa aca tac ttt cga ttt cag gag gaa ata aaa gaa aac aca			690
Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr			
185	190	195	200
aag aac gac aaa caa atg gtc caa tat att tac aaa tac aca agt tat			738
Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr			
205	210	215	
cct gac cct ata ttg ttg atg aaa agt gct aga aat agt tgt tgg tct			786
Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser			
220	225	230	
aaa gat gca gaa tat gga ctc tat tcc atc tat caa ggg gga ata ttt			834
Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe			
235	240	245	
gag ctt aag gaa aat gac aga att ttt gtt tct gta aca aat gag cac			882
Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His			
250	255	260	
ttg ata gac atg gac cat gaa gcc agt ttt ttc ggg gcc ttt tta gtt			930
Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val			
265	270	275	280
ggc taa ctgacctgga aagaaaaagc aataacctca aagtgactat tcagttttca			986
Gly			
ggatgataca ctatgaagat gtttcaaaaa atctgaccaa aacaaacaaa cagaaa			1042

<210> 24

<211> 281

<212> PRT

<213> Homo sapiens

<400> 24

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1 5 10 15

Val Leu Ile Val Ile Phe Thr Val Leu Leu Gln Ser Leu Cys Val Ala
20 25 30

Val Thr Tyr Val Tyr Phe Thr Asn Glu Leu Lys Gln Met Gln Asp Lys
35 40 45

Tyr Ser Lys Ser Gly Ile Ala Cys Phe Leu Lys Glu Asp Asp Ser Tyr
50 55 60

Trp Asp Pro Asn Asp Glu Glu Ser Met Asn Ser Pro Cys Trp Gln Val
65 70 75 80

Lys Trp Gln Leu Arg Gln Leu Val Arg Lys Met Ile Leu Arg Thr Ser
85 90 95

Glu Glu Thr Ile Ser Thr Val Gln Glu Lys Gln Gln Asn Ile Ser Pro
100 105 110

Leu Val Arg Glu Arg Gly Pro Gln Arg Val Ala Ala His Ile Thr Gly
115 120 125

Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu
130 135 140

Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly
145 150 155 160

His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val Ile
165 170 175

His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe
180 185 190

Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val Gln
195 200 205

Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys
210 215 220

Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr
225 230 235 240

Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile

245	250	255
Phe Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu Ala		
260	265	270

Ser Phe Phe Gly Ala Phe Leu Val Gly
275 280

<210> 25
 <211> 579
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(579)

<400> 25

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Met Asp Gly Ser Gly Glu Gln Pro Arg Gly Gly Gly Pro Thr Ser Ser	
1 5 10 15	
 gag cag atc atg aag aca ggg gcc ctt ttg ctt cag ggt ttc atc cag	96
Glu Gln Ile Met Lys Thr Gly Ala Leu Leu Leu Gln Gly Phe Ile Gln	
20 25 30	
 gat cga gca ggg cga atg ggg ggg gag gca ccc gag ctg gcc ctg gac	144
Asp Arg Ala Gly Arg Met Gly Gly Glu Ala Pro Glu Leu Ala Leu Asp	
35 40 45	
 ccg gtg cct cag gat gcg tcc acc aag aag ctg agc gag tgt ctc aag	192
Pro Val Pro Gln Asp Ala Ser Thr Lys Lys Leu Ser Glu Cys Leu Lys	
50 55 60	
 cgc atc ggg gac gaa ctg gac agt aac atg gag ctg cag agg atg att	240
Arg Ile Gly Asp Glu Leu Asp Ser Asn Met Glu Leu Gln Arg Met Ile	
65 70 75 80	
 gcc gcc gtg gac aca gac tcc ccc cga gag gtc ttt ttc cga gtg gca	288
Ala Ala Val Asp Thr Asp Ser Pro Arg Glu Val Phe Phe Arg Val Ala	
85 90 95	
 gct gac atg ttt tct gac ggc aac ttc aac tgg ggc cgg gtt gtc gcc	336
Ala Asp Met Phe Ser Asp Gly Asn Phe Asn Trp Gly Arg Val Val Ala	
100 105 110	
 ctt ttc tac ttt gcc agc aaa ctg gtg ctc aag gcc ctg tgc acc aag	384

Leu	Phe	Tyr	Phe	Ala	Ser	Lys	Leu	Val	Leu	Lys	Ala	Leu	Cys	Thr	Lys		
	115						120					125					
gtg	ccg	gaa	ctg	atc	aga	acc	atc	atg	ggc	tgg	aca	ttg	gac	ttc	ctc	432	
Val	Pro	Glu	Leu	Ile	Arg	Thr	Ile	Met	Gly	Trp	Thr	Leu	Asp	Phe	Leu		
	130					135					140						
cgg	gag	cgg	ctg	ttg	ggc	tgg	atc	caa	gac	cag	ggg	ggg	tgg	gac	ggc	480	
Arg	Glu	Arg	Leu	Leu	Gly	Trp	Ile	Gln	Asp	Gln	Gly	Gly	Trp	Asp	Gly		
145					150					155					160		
ctc	ctc	tcc	tac	ttt	ggg	acg	ccc	acg	tgg	cag	acc	gtg	acc	atc	ttt	528	
Leu	Leu	Ser	Tyr	Phe	Gly	Thr	Pro	Thr	Trp	Gln	Thr	Val	Thr	Ile	Phe		
				165					170					175			
gtg	gcg	gga	gtg	ctc	acc	gcc	tcg	ctc	acc	atc	tgg	aag	aag	atg	ggc	576	
Val	Ala	Gly	Val	Leu	Thr	Ala	Ser	Leu	Thr	Ile	Trp	Lys	Lys	Met	Gly		
			180					185					190				
tga																579	

<210> 26

<211> 192

<212> PRT

<213> Homo sapiens

<400> 26

Met	Asp	Gly	Ser	Gly	Glu	Gln	Pro	Arg	Gly	Gly	Gly	Pro	Thr	Ser	Ser		
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Glu	Gln	Ile	Met	Lys	Thr	Gly	Ala	Leu	Leu	Leu	Gln	Gly	Phe	Ile	Gln		
			20					25					30				
Asp	Arg	Ala	Gly	Arg	Met	Gly	Gly	Glu	Ala	Pro	Glu	Leu	Ala	Leu	Asp		
		35				40						45					
Pro	Val	Pro	Gln	Asp	Ala	Ser	Thr	Lys	Lys	Leu	Ser	Glu	Cys	Leu	Lys		
	50					55					60						
Arg	Ile	Gly	Asp	Glu	Leu	Asp	Ser	Asn	Met	Glu	Leu	Gln	Arg	Met	Ile		
65					70					75					80		
Ala	Ala	Val	Asp	Thr	Asp	Ser	Pro	Arg	Glu	Val	Phe	Phe	Arg	Val	Ala		
				85					90					95			
Ala	Asp	Met	Phe	Ser	Asp	Gly	Asn	Phe	Asn	Trp	Gly	Arg	Val	Val	Ala		

100	105	110
Leu Phe Tyr Phe Ala Ser Lys Leu Val Leu Lys Ala Leu Cys Thr Lys		
115	120	125
Val Pro Glu Leu Ile Arg Thr Ile Met Gly Trp Thr Leu Asp Phe Leu		
130	135	140
Arg Glu Arg Leu Leu Gly Trp Ile Gln Asp Gln Gly Gly Trp Asp Gly		
145	150	155
		160
Leu Leu Ser Tyr Phe Gly Thr Pro Thr Trp Gln Thr Val Thr Ile Phe		
165	170	175
Val Ala Gly Val Leu Thr Ala Ser Leu Thr Ile Trp Lys Lys Met Gly		
180	185	190

<210> 27
 <211> 1105
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (141)..(728)

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gcgccccgcg ggctggaggg tggtegccac tgggacactg tgaaccagga gtgagtcgga 120

gctgccgcgc tgcccaggcc atg gac tgt gag gtc aac aac ggt tcc agc ctc 173
 Met Asp Cys Glu Val Asn Asn Gly Ser Ser Leu
 1 5 10

agg gat gag tgc atc aca aac cta ctg gtg ttt ggc ttc ctc caa agc 221
 Arg Asp Glu Cys Ile Thr Asn Leu Leu Val Phe Gly Phe Leu Gln Ser
 15 20 25

tgt tct gac aac agc ttc cgc aga gag ctg gac gca ctg ggc cac gag 269
 Cys Ser Asp Asn Ser Phe Arg Arg Glu Leu Asp Ala Leu Gly His Glu
 30 35 40

ctg cca gtg ctg gct ccc cag tgg gag ggc tac gat gag ctg cag act 317
 Leu Pro Val Leu Ala Pro Gln Trp Glu Gly Tyr Asp Glu Leu Gln Thr
 45 50 55

gat ggc aac cgc agc agc cac tcc cgc ttg gga aga ata gag gca gat	365
Asp Gly Asn Arg Ser Ser His Ser Arg Leu Gly Arg Ile Glu Ala Asp	
60 65 70 75	
tct gaa agt caa gaa gac atc atc cgg aat att gcc agg cac ctc gcc	413
Ser Glu Ser Gln Glu Asp Ile Ile Arg Asn Ile Ala Arg His Leu Ala	
80 85 90	
cag gtc ggg gac agc atg gac cgt agc atc cct ccg ggc ctg gtg aac	461
Gln Val Gly Asp Ser Met Asp Arg Ser Ile Pro Pro Gly Leu Val Asn	
95 100 105	
ggc ctg gcc ctg cag ctc agg aac acc agc cgg tcg gag gag gac cgg	509
Gly Leu Ala Leu Gln Leu Arg Asn Thr Ser Arg Ser Glu Glu Asp Arg	
110 115 120	
aac agg gac ctg gcc act gcc ctg gag cag ctg ctg cag gcc tac cct	557
Asn Arg Asp Leu Ala Thr Ala Leu Glu Gln Leu Leu Gln Ala Tyr Pro	
125 130 135	
aga gac atg gag aag gag aag acc atg ctg gtg ctg gcc ctg ctg ctg	605
Arg Asp Met Glu Lys Glu Lys Thr Met Leu Val Leu Ala Leu Leu Leu	
140 145 150 155	
gcc aag aag gtg gcc agt cac acg ccg tcc ttg ctc cgt gat gtc ttt	653
Ala Lys Lys Val Ala Ser His Thr Pro Ser Leu Leu Arg Asp Val Phe	
160 165 170	
cac aca aca gtg aat ttt att aac cag aac cta cgc acc tac gtg agg	701
His Thr Thr Val Asn Phe Ile Asn Gln Asn Leu Arg Thr Tyr Val Arg	
175 180 185	
agc tta gcc aga aat ggg atg gac tga acggacagtt ccagaagtgt	748
Ser Leu Ala Arg Asn Gly Met Asp	
190 195	
gactggctaa agcttgatgt ggtcacagct gtatagctgc ttccagtgtgac gacggagccc 808	
tggcatgtca acagcgttcc tagagaagac aggctggaag atagctgtga cttctatattt 868	
aaagacaatg ttaaacttat aaccactttt aaaatatcta cattaatata cttgaatgaa 928	
aatgtccatt tacacgtatt tgaatggcct tcatatcatc cacacatgaa tctgcacatc 988	
tgtaaactta cacacgggtgc ctttattttcc actgtgcagg ttccactta aaaattaaat 1048	
tggaagcag gtttcaagga agtagaaaca aaatacaatt tttttggtaa aaaaaa 1105	

<210> 28

<211> 195

<212> PRT

<213> Homo sapiens

<400> 28

Met Asp Cys Glu Val Asn Asn Gly Ser Ser Leu Arg Asp Glu Cys Ile
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Thr Asn Leu Leu Val Phe Gly Phe Leu Gln Ser Cys Ser Asp Asn Ser
20 25 30

Phe Arg Arg Glu Leu Asp Ala Leu Gly His Glu Leu Pro Val Leu Ala
35 40 45

Pro Gln Trp Glu Gly Tyr Asp Glu Leu Gln Thr Asp Gly Asn Arg Ser
50 55 60

Ser His Ser Arg Leu Gly Arg Ile Glu Ala Asp Ser Glu Ser Gln Glu
65 70 75 80

Asp Ile Ile Arg Asn Ile Ala Arg His Leu Ala Gln Val Gly Asp Ser
85 90 95

Met Asp Arg Ser Ile Pro Pro Gly Leu Val Asn Gly Leu Ala Leu Gln
100 105 110

Leu Arg Asn Thr Ser Arg Ser Glu Glu Asp Arg Asn Arg Asp Leu Ala
115 120 125

Thr Ala Leu Glu Gln Leu Leu Gln Ala Tyr Pro Arg Asp Met Glu Lys
130 135 140

Glu Lys Thr Met Leu Val Leu Ala Leu Leu Leu Ala Lys Lys Val Ala
145 150 155 160

Ser His Thr Pro Ser Leu Leu Arg Asp Val Phe His Thr Thr Val Asn
165 170 175

Phe Ile Asn Gln Asn Leu Arg Thr Tyr Val Arg Ser Leu Ala Arg Asn
180 185 190

Gly Met Asp
195

<210> 29

<211> 923
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (26)..(508)

<400> 29

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                          1                      5

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Asp Ile Leu Met Glu Thr Leu Leu Tyr Glu Gln Leu Leu Glu Pro Pro
 10                      15                      20                      25

acc atg gag gtt ctt ggc atg act gac tct gaa gag gac ctg gac cct 148
Thr Met Glu Val Leu Gly Met Thr Asp Ser Glu Glu Asp Leu Asp Pro
                      30                      35                      40

atg gag gac ttc gat tct ttg gaa tgc atg gag ggc agt gac gca ttg 196
Met Glu Asp Phe Asp Ser Leu Glu Cys Met Glu Gly Ser Asp Ala Leu
                      45                      50                      55

gcc ctg cgg ctg gcc tgc atc ggg gac gag atg gac gtg agc ctc agg 244
Ala Leu Arg Leu Ala Cys Ile Gly Asp Glu Met Asp Val Ser Leu Arg
                      60                      65                      70

gcc ccg cgc ctg gcc cag ctc tcc gag gtg gcc atg cac agc ctg ggt 292
Ala Pro Arg Leu Ala Gln Leu Ser Glu Val Ala Met His Ser Leu Gly
                      75                      80                      85

ctg gct ttc atc tac gac cag act gag gac atc agg gat gtt ctt aga 340
Leu Ala Phe Ile Tyr Asp Gln Thr Glu Asp Ile Arg Asp Val Leu Arg
 90                      95                      100                      105

agt ttc atg gac ggt ttc acc aca ctt aag gag aac ata atg agg ttc 388
Ser Phe Met Asp Gly Phe Thr Thr Leu Lys Glu Asn Ile Met Arg Phe
                      110                      115                      120

tgg aga tcc ccg aac ccc ggg tcc tgg gtg tcc tgc gaa cag gtg ctg 436
Trp Arg Ser Pro Asn Pro Gly Ser Trp Val Ser Cys Glu Gln Val Leu
                      125                      130                      135

ctg gcg ctg ctg ctg ctg ctg gcg ctg ctg ctg ccg ctg ctc agc ggg 484
Leu Ala Leu Leu Leu Leu Leu Ala Leu Leu Leu Pro Leu Leu Ser Gly
                      140                      145                      150

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ggc ctg cac ctg ctg ctc aag tga gcccccgcg gctcaggcgt ggctggcccc 538
 Gly Leu His Leu Leu Leu Lys
 155 160

accccatga ccactgcct gaggtggcgg cctgctgctg ttatcttttt aactgttttc 598
 tcatgatgcc ttttatatta acccgtgat agtgctggaa cactgctgag gttttatact 658
 caggtttttt gttttttttt tattccagtt ttcgtttttt ctaaaagatg aattcctatg 718
 gctctgcaat tgtcacccgg taactgtggc ctgtgccag gaagagccat tcactcctgc 778
 ccctgccac acggcaggta gcagggggag tgctggtcac acccctgtgt gatatgtgat 838
 gccctcggca aagaatctac tggaatagat tccgaggagc aggagtgctc aataaaatgt 898
 tggtttccag caaaaaaaaa aaaaa 923

<210> 30
 <211> 160
 <212> PRT
 <213> Homo sapiens

<400> 30
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 Leu Tyr Glu Gln Leu Leu Glu Pro Pro Thr Met Glu Val Leu Gly Met
 20 25 30
 Thr Asp Ser Glu Glu Asp Leu Asp Pro Met Glu Asp Phe Asp Ser Leu
 35 40 45
 Glu Cys Met Glu Gly Ser Asp Ala Leu Ala Leu Arg Leu Ala Cys Ile
 50 55 60
 Gly Asp Glu Met Asp Val Ser Leu Arg Ala Pro Arg Leu Ala Gln Leu
 65 70 75 80
 Ser Glu Val Ala Met His Ser Leu Gly Leu Ala Phe Ile Tyr Asp Gln
 85 90 95
 Thr Glu Asp Ile Arg Asp Val Leu Arg Ser Phe Met Asp Gly Phe Thr
 100 105 110
 Thr Leu Lys Glu Asn Ile Met Arg Phe Trp Arg Ser Pro Asn Pro Gly

115	120	125	
Ser Trp Val Ser Cys Glu Gln Val Leu Leu Ala Leu Leu Leu Leu Leu			
130	135	140	
Ala Leu Leu Leu Pro Leu Leu Ser Gly Gly Leu His Leu Leu Leu Lys			
145	150	155	160
<210> 31			
<211> 507			
<212> DNA			
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<221> CDS			
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<400> 31			
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1 5 10 15			
tct gca gag agg ggc ctg ggc ccc agc ccc gca ggg gac ggg ccc tca	96		
Ser Ala Glu Arg Gly Leu Gly Pro Ser Pro Ala Gly Asp Gly Pro Ser			
20 25 30			
ggc tcc ggc aag cat cat cgc cag gcc cca ggc ctc ctg tgg gac gcc	144		
Gly Ser Gly Lys His His Arg Gln Ala Pro Gly Leu Leu Trp Asp Ala			
35 40 45			
agt cac cag cag gag cag cca acc agc agc agc cat cat gga ggc gct	192		
Ser His Gln Gln Glu Gln Pro Thr Ser Ser Ser His His Gly Gly Ala			
50 55 60			
ggg gct gtg gag atc cgg agt cgc cac agc tcc tac ccc gcg ggg acg	240		
Gly Ala Val Glu Ile Arg Ser Arg His Ser Ser Tyr Pro Ala Gly Thr			
65 70 75 80			
gag gac gac gaa ggg atg ggg gag gag ccc agc ccc ttt cgg ggc cgc	288		
Glu Asp Asp Glu Gly Met Gly Glu Glu Pro Ser Pro Phe Arg Gly Arg			
85 90 95			
tcg cgc tcg gcg ccc ccc aac ctc tgg gca gca cag cgc tat ggc cgc	336		
Ser Arg Ser Ala Pro Pro Asn Leu Trp Ala Ala Gln Arg Tyr Gly Arg			
100 105 110			
gag ctc cgg agg atg agt gac gag ttt gtg gac tcc ttt aag aag gga	384		

Glu Leu Arg Arg Met Ser Asp Glu Phe Val Asp Ser Phe Lys Lys Gly
 115 120 125

ctt cct cgc ccg aag agc gcg ggc aca gca acg cag atg cgg caa agc 432
 Leu Pro Arg Pro Lys Ser Ala Gly Thr Ala Thr Gln Met Arg Gln Ser
 130 135 140

tcc agc tgg acg cga gtc ttc cag tcc tgg tgg gat cgg aac ttg ggc 480
 Ser Ser Trp Thr Arg Val Phe Gln Ser Trp Trp Asp Arg Asn Leu Gly
 145 150 155 160

agg gga agc tcc gcc ccc tcc cag tga 507
 Arg Gly Ser Ser Ala Pro Ser Gln
 165

<210> 32
 <211> 168
 <212> PRT
 <213> Homo sapiens

<400> 32
 Met Phe Gln Ile Pro Glu Phe Glu Pro Ser Glu Gln Glu Asp Ser Ser
 1 5 10 15

Ser Ala Glu Arg Gly Leu Gly Pro Ser Pro Ala Gly Asp Gly Pro Ser
 20 25 30

Gly Ser Gly Lys His His Arg Gln Ala Pro Gly Leu Leu Trp Asp Ala
 35 40 45

Ser His Gln Gln Glu Gln Pro Thr Ser Ser Ser His His Gly Gly Ala
 50 55 60

Gly Ala Val Glu Ile Arg Ser Arg His Ser Ser Tyr Pro Ala Gly Thr
 65 70 75 80

Glu Asp Asp Glu Gly Met Gly Glu Glu Pro Ser Pro Phe Arg Gly Arg
 85 90 95

Ser Arg Ser Ala Pro Pro Asn Leu Trp Ala Ala Gln Arg Tyr Gly Arg
 100 105 110

Glu Leu Arg Arg Met Ser Asp Glu Phe Val Asp Ser Phe Lys Lys Gly
 115 120 125

Leu Pro Arg Pro Lys Ser Ala Gly Thr Ala Thr Gln Met Arg Gln Ser
 130 135 140

Ser Ser Trp Thr Arg Val Phe Gln Ser Trp Trp Asp Arg Asn Leu Gly
 145 150 155 160

Arg Gly Ser Ser Ala Pro Ser Gln
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<210> 33

<211> 1949

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (65)..(700)

<400> 33

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aaaa atg gct tcg ggg caa ggc cca ggt cct ccc agg cag gag tgc gga 109
 Met Ala Ser Gly Gln Gly Pro Gly Pro Pro Arg Gln Glu Cys Gly
 1 5 10 15

gag cct gcc ctg ccc tct gct tct gag gag cag gta gcc cag gac aca 157
 Glu Pro Ala Leu Pro Ser Ala Ser Glu Glu Gln Val Ala Gln Asp Thr
 20 25 30

gag gag gtt ttc cgc agc tac gtt ttt tac cgc cat cag cag gaa cag 205
 Glu Glu Val Phe Arg Ser Tyr Val Phe Tyr Arg His Gln Gln Glu Gln
 35 40 45

gag gct gaa ggg gtg gct gcc cct gcc gac cca gag atg gtc acc tta 253
 Glu Ala Glu Gly Val Ala Ala Pro Ala Asp Pro Glu Met Val Thr Leu
 50 55 60

cct ctg caa cct agc agc acc atg ggg cag gtg gga cgg cag ctc gcc 301
 Pro Leu Gln Pro Ser Ser Thr Met Gly Gln Val Gly Arg Gln Leu Ala
 65 70 75

atc atc ggg gac gac atc aac cga cgc tat gac tca gag ttc cag acc 349
 Ile Ile Gly Asp Asp Ile Asn Arg Arg Tyr Asp Ser Glu Phe Gln Thr
 80 85 90 95

atg ttg cag cac ctg cag ccc acg gca gag aat gcc tat gag tac ttc 397
 Met Leu Gln His Leu Gln Pro Thr Ala Glu Asn Ala Tyr Glu Tyr Phe
 100 105 110

acc aag att gcc acc agc ctg ttt gag agt ggc atc aat tgg ggc cgt 445
 Thr Lys Ile Ala Thr Ser Leu Phe Glu Ser Gly Ile Asn Trp Gly Arg
 115 120 125

gtg gtg gct ctt ctg ggc ttc ggc tac cgt ctg gcc cta cac gtc tac 493
 Val Val Ala Leu Leu Gly Phe Gly Tyr Arg Leu Ala Leu His Val Tyr
 130 135 140

cag cat ggc ctg act ggc ttc cta ggc cag gtg acc cgc ttc gtg gtc 541
 Gln His Gly Leu Thr Gly Phe Leu Gly Gln Val Thr Arg Phe Val Val
 145 150 155

gac ttc atg ctg cat cac tgc att gcc cgg tgg att gca cag agg ggt 589
 Asp Phe Met Leu His His Cys Ile Ala Arg Trp Ile Ala Gln Arg Gly
 160 165 170 175

ggc tgg gtg gca gcc ctg aac ttg ggc aat ggt ccc atc ctg aac gtg 637
 Gly Trp Val Ala Ala Leu Asn Leu Gly Asn Gly Pro Ile Leu Asn Val
 180 185 190

ctg gtg gtt ctg ggt gtg gtt ctg ttg ggc cag ttt gtg gta cga aga 685
 Leu Val Val Leu Gly Val Val Leu Leu Gly Gln Phe Val Val Arg Arg
 195 200 205

ttc ttc aaa tca tga ctcccaaggg tgccttttgg gtcccgggttc agaccctgc 740
 Phe Phe Lys Ser
 210

ctggacttaa gogaagtctt tgccttctct gtcccttgc aggggtcccc cctcaagagt 800

acagaagctt tagcaagtgt gcactccagc ttcggagggc cctgcgtgg gggccagtca 860

ggctgcagag gcacctcaac attgcatggt gctagtgggc cctctctctg ggcccagggg 920

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ccaggacgtc tggggtgtgg ggattggtgg gtctatgttc ccaggattc agctattctg 1160

gaagatcagc accctaagag atgggactag gacctgagcc tggctctggc cgtccctaag 1220

catgtgtccc aggagcagga cctactagga gagggggggc aaggctctgc tcaactctac 1280

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 atccctca 1949

<210> 34
 <211> 211
 <212> PRT
 <213> Homo sapiens

<400> 34

Met	Ala	Ser	Gly	Gln	Gly	Pro	Gly	Pro	Pro	Arg	Gln	Glu	Cys	Gly	Glu
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			20					25					30		
Glu	Val	Phe	Arg	Ser	Tyr	Val	Phe	Tyr	Arg	His	Gln	Gln	Glu	Gln	Glu
		35					40					45			
Ala	Glu	Gly	Val	Ala	Ala	Pro	Ala	Asp	Pro	Glu	Met	Val	Thr	Leu	Pro
	50					55				60					
Leu	Gln	Pro	Ser	Ser	Thr	Met	Gly	Gln	Val	Gly	Arg	Gln	Leu	Ala	Ile
65					70					75				80	
Ile	Gly	Asp	Asp	Ile	Asn	Arg	Arg	Tyr	Asp	Ser	Glu	Phe	Gln	Thr	Met
				85				90					95		
Leu	Gln	His	Leu	Gln	Pro	Thr	Ala	Glu	Asn	Ala	Tyr	Glu	Tyr	Phe	Thr

100	105	110
Lys Ile Ala Thr Ser Leu Phe Glu Ser Gly Ile Asn Trp Gly Arg Val		
115	120	125
Val Ala Leu Leu Gly Phe Gly Tyr Arg Leu Ala Leu His Val Tyr Gln		
130	135	140
His Gly Leu Thr Gly Phe Leu Gly Gln Val Thr Arg Phe Val Val Asp		
145	150	155
		160
Phe Met Leu His His Cys Ile Ala Arg Trp Ile Ala Gln Arg Gly Gly		
	165	170
		175
Trp Val Ala Ala Leu Asn Leu Gly Asn Gly Pro Ile Leu Asn Val Leu		
	180	185
		190
Val Val Leu Gly Val Val Leu Leu Gly Gln Phe Val Val Arg Arg Phe		
	195	200
		205
Phe Lys Ser		
210		

<210> 35
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 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (225)..(1847)

<400> 35
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 catccgggga atgggcgccc tcgtgaccta gtgttgccgg gcaaaaagg tcttgccggc 120
 ctcgctcgtg caggggcgta tctgggcgcc tgagcgcgca gtgggagcct tgggagccgc 180
 cgcagcaggg ggcacacccg gaaccggcct gagcgcccgg gacc atg aac ggg gag 236
 Met Asn Gly Glu

1

gcc atc tgc agc gcc ctg ccc acc att ccc tac cac aaa ctc gcc gac 284
 Ala Ile Cys Ser Ala Leu Pro Thr Ile Pro Tyr His Lys Leu Ala Asp
 5 10 15 20

ctg cgc tac ctg agc cgc ggc gcc tct ggc act gtg tcg tcc gcc cgc	332
Leu Arg Tyr Leu Ser Arg Gly Ala Ser Gly Thr Val Ser Ser Ala Arg	
25 30 35	
cac gca gac tgg cgc gtc cag gtg gcc gtg aag cac ctg cac atc cac	380
His Ala Asp Trp Arg Val Gln Val Ala Val Lys His Leu His Ile His	
40 45 50	
act ccg ctg ctc gac agt gaa aga aag gat gtc tta aga gaa gct gaa	428
Thr Pro Leu Leu Asp Ser Glu Arg Lys Asp Val Leu Arg Glu Ala Glu	
55 60 65	
att tta cac aaa gct aga ttt agt tac att ctt cca att ttg gga att	476
Ile Leu His Lys Ala Arg Phe Ser Tyr Ile Leu Pro Ile Leu Gly Ile	
70 75 80	
tgc aat gag cct gaa ttt ttg gga ata gtt act gaa tac atg cca aat	524
Cys Asn Glu Pro Glu Phe Leu Gly Ile Val Thr Glu Tyr Met Pro Asn	
85 90 95 100	
gga tca tta aat gaa ctc cta cat agg aaa act gaa tat cct gat gtt	572
Gly Ser Leu Asn Glu Leu Leu His Arg Lys Thr Glu Tyr Pro Asp Val	
105 110 115	
gct tgg cca ttg aga ttt cgc atc ctg cat gaa att gcc ctt ggt gta	620
Ala Trp Pro Leu Arg Phe Arg Ile Leu His Glu Ile Ala Leu Gly Val	
120 125 130	
aat tac ctg cac aat atg act cct cct tta ctt cat cat gac ttg aag	668
Asn Tyr Leu His Asn Met Thr Pro Pro Leu Leu His His Asp Leu Lys	
135 140 145	
act cag aat atc tta ttg gac aat gaa ttt cat gtt aag att gca gat	716
Thr Gln Asn Ile Leu Leu Asp Asn Glu Phe His Val Lys Ile Ala Asp	
150 155 160	
ttt ggt tta tca aag tgg cgc atg atg tcc ctc tca cag tca cga agt	764
Phe Gly Leu Ser Lys Trp Arg Met Met Ser Leu Ser Gln Ser Arg Ser	
165 170 175 180	
agc aaa tct gca cca gaa gga ggg aca att atc tat atg cca cct gaa	812
Ser Lys Ser Ala Pro Glu Gly Gly Thr Ile Ile Tyr Met Pro Pro Glu	
185 190 195	
aac tat gaa cct gga caa aaa tca agg gcc agt atc aag cac gat ata	860
Asn Tyr Glu Pro Gly Gln Lys Ser Arg Ala Ser Ile Lys His Asp Ile	
200 205 210	

tat agc tat gca gtt atc aca tgg gaa gtg tta tcc aga aaa cag cct	908
Tyr Ser Tyr Ala Val Ile Thr Trp Glu Val Leu Ser Arg Lys Gln Pro	
215 220 225	
ttt gaa gat gtc acc aat cct ttg cag ata atg tat agt gtg tca caa	956
Phe Glu Asp Val Thr Asn Pro Leu Gln Ile Met Tyr Ser Val Ser Gln	
230 235 240	
gga cat cga cct gtt att aat gaa gaa agt ttg cca tat gat ata cct	1004
Gly His Arg Pro Val Ile Asn Glu Glu Ser Leu Pro Tyr Asp Ile Pro	
245 250 255 260	
cac cga gca cgt atg atc tct cta ata gaa agt gga tgg gca caa aat	1052
His Arg Ala Arg Met Ile Ser Leu Ile Glu Ser Gly Trp Ala Gln Asn	
265 270 275	
cca gat gaa aga cca tct ttc tta aaa tgt tta ata gaa ctt gaa cca	1100
Pro Asp Glu Arg Pro Ser Phe Leu Lys Cys Leu Ile Glu Leu Glu Pro	
280 285 290	
gtt ttg aga aca ttt gaa gag ata act ttt ctt gaa gct gtt att cag	1148
Val Leu Arg Thr Phe Glu Glu Ile Thr Phe Leu Glu Ala Val Ile Gln	
295 300 305	
cta aag aaa aca aag tta cag agt gtt tca agt gcc att cac cta tgt	1196
Leu Lys Lys Thr Lys Leu Gln Ser Val Ser Ser Ala Ile His Leu Cys	
310 315 320	
gac aag aag aaa atg gaa tta tct ctg aac ata cct gta aat cat ggt	1244
Asp Lys Lys Lys Met Glu Leu Ser Leu Asn Ile Pro Val Asn His Gly	
325 330 335 340	
cca caa gag gaa tca tgt gga tcc tct cag ctc cat gaa aat agt ggt	1292
Pro Gln Glu Glu Ser Cys Gly Ser Ser Gln Leu His Glu Asn Ser Gly	
345 350 355	
tct cct gaa act tca agg tcc ctg cca gct cct caa gac aat gat ttt	1340
Ser Pro Glu Thr Ser Arg Ser Leu Pro Ala Pro Gln Asp Asn Asp Phe	
360 365 370	
tta tct aga aaa gct caa gac tgt tat ttt atg aag ctg cat cac tgt	1388
Leu Ser Arg Lys Ala Gln Asp Cys Tyr Phe Met Lys Leu His His Cys	
375 380 385	
cct gga aat cac agt tgg gat agc acc att tct ggt tct caa agg gct	1436
Pro Gly Asn His Ser Trp Asp Ser Thr Ile Ser Gly Ser Gln Arg Ala	
390 395 400	

gca ttc tgt gat cac aag acc act cca tgc tct tca gca ata ata aat 1484
Ala Phe Cys Asp His Lys Thr Thr Pro Cys Ser Ser Ala Ile Ile Asn
405 410 415 420

cca ctc tca act gca gga aac tca gaa cgt ctg cag cct ggt ata gcc 1532
Pro Leu Ser Thr Ala Gly Asn Ser Glu Arg Leu Gln Pro Gly Ile Ala
425 430 435

cag cag tgg atc cag agc aaa agg gaa gac att gtg aac caa atg aca 1580
Gln Gln Trp Ile Gln Ser Lys Arg Glu Asp Ile Val Asn Gln Met Thr
440 445 450

gaa gcc tgc ctt aac cag tcg cta gat gcc ctt ctg tcc agg gac ttg 1628
Glu Ala Cys Leu Asn Gln Ser Leu Asp Ala Leu Leu Ser Arg Asp Leu
455 460 465

atc atg aaa gag gac tat gaa ctt gtt agt acc aag cct aca agg acc 1676
Ile Met Lys Glu Asp Tyr Glu Leu Val Ser Thr Lys Pro Thr Arg Thr
470 475 480

tca aaa gtc aga caa tta cta gac act act gac atc caa gga gaa gaa 1724
Ser Lys Val Arg Gln Leu Leu Asp Thr Thr Asp Ile Gln Gly Glu Glu
485 490 495 500

ttt gcc aaa gtt ata gta caa aaa ttg aaa gat aac aaa caa atg ggt 1772
Phe Ala Lys Val Ile Val Gln Lys Leu Lys Asp Asn Lys Gln Met Gly
505 510 515

ctt cag cct tac ccg gaa ata ctt gtg gtt tct aga tca cca tct tta 1820
Leu Gln Pro Tyr Pro Glu Ile Leu Val Val Ser Arg Ser Pro Ser Leu
520 525 530

aat tta ctt caa aat aaa agc atg taa gtgactgttt ttcaagaaga 1867
Asn Leu Leu Gln Asn Lys Ser Met
535 540

aatgtgtttc ataaaaggat atttatatct ctgttgcttt gacttttttt atataaaatc 1927

cgtgagtatt aaagctttat tgaaggttct ttgggtaaat attagtctcc ctccatgaca 1987

ctgcagtatt ttttttaatt aatacaagta aaaagttgaa tttggttgaa tttgctacat 2047

agttcaatth ttatgtctct tttgttaaca gaaaccactt ttaaaggata gtaattatc 2107

ttgtttataa cagtgcctta aggtatgatg tatttctgat ggaagccatt ttcacattca 2167

tgttcttcat ggattatthg ttacttgtct aagatgcaat ttgattttat gaagtatata 2227

ccctttaccc accagagaca gtacagaatc cctgccctaa aatcccaggc ttaattgccc 2287
 tacaaaggggt tattaattta aaactccatt attaggatta catttttaaag ttttatttat 2347
 gaattccctt taaaaatgat atttcaaagg taaaacaata caatataaag aaaaaaataa 2407
 atatattaat accggcttcc tgtccccatt tttaacctca gccttccta ctgtcaccaa 2467
 caaccaagct aaataaagtc aacagcctga tgtg 2501

<210> 36
 <211> 540
 <212> PRT
 <213> Homo sapiens

<400> 36

Met Asn Gly Glu Ala Ile Cys Ser Ala Leu Pro Thr Ile Pro Tyr His
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Lys Leu Ala Asp Leu Arg Tyr Leu Ser Arg Gly Ala Ser Gly Thr Val
 20 25 30

Ser Ser Ala Arg His Ala Asp Trp Arg Val Gln Val Ala Val Lys His
 35 40 45

Leu His Ile His Thr Pro Leu Leu Asp Ser Glu Arg Lys Asp Val Leu
 50 55 60

Arg Glu Ala Glu Ile Leu His Lys Ala Arg Phe Ser Tyr Ile Leu Pro
 65 70 75 80

Ile Leu Gly Ile Cys Asn Glu Pro Glu Phe Leu Gly Ile Val Thr Glu
 85 90 95

Tyr Met Pro Asn Gly Ser Leu Asn Glu Leu Leu His Arg Lys Thr Glu
 100 105 110

Tyr Pro Asp Val Ala Trp Pro Leu Arg Phe Arg Ile Leu His Glu Ile
 115 120 125

Ala Leu Gly Val Asn Tyr Leu His Asn Met Thr Pro Pro Leu Leu His
 130 135 140

His Asp Leu Lys Thr Gln Asn Ile Leu Leu Asp Asn Glu Phe His Val
 145 150 155 160

Lys Ile Ala Asp Phe Gly Leu Ser Lys Trp Arg Met Met Ser Leu Ser

	165		170		175
Gln Ser Arg Ser Ser Lys Ser Ala Pro Glu Gly Gly Thr Ile Ile Tyr					
	180		185		190
Met Pro Pro Glu Asn Tyr Glu Pro Gly Gln Lys Ser Arg Ala Ser Ile					
	195		200		205
Lys His Asp Ile Tyr Ser Tyr Ala Val Ile Thr Trp Glu Val Leu Ser					
	210		215		220
Arg Lys Gln Pro Phe Glu Asp Val Thr Asn Pro Leu Gln Ile Met Tyr					
	225		230		235
Ser Val Ser Gln Gly His Arg Pro Val Ile Asn Glu Glu Ser Leu Pro					
	245		250		255
Tyr Asp Ile Pro His Arg Ala Arg Met Ile Ser Leu Ile Glu Ser Gly					
	260		265		270
Trp Ala Gln Asn Pro Asp Glu Arg Pro Ser Phe Leu Lys Cys Leu Ile					
	275		280		285
Glu Leu Glu Pro Val Leu Arg Thr Phe Glu Glu Ile Thr Phe Leu Glu					
	290		295		300
Ala Val Ile Gln Leu Lys Lys Thr Lys Leu Gln Ser Val Ser Ser Ala					
	305		310		315
Ile His Leu Cys Asp Lys Lys Lys Met Glu Leu Ser Leu Asn Ile Pro					
	325		330		335
Val Asn His Gly Pro Gln Glu Glu Ser Cys Gly Ser Ser Gln Leu His					
	340		345		350
Glu Asn Ser Gly Ser Pro Glu Thr Ser Arg Ser Leu Pro Ala Pro Gln					
	355		360		365
Asp Asn Asp Phe Leu Ser Arg Lys Ala Gln Asp Cys Tyr Phe Met Lys					
	370		375		380
Leu His His Cys Pro Gly Asn His Ser Trp Asp Ser Thr Ile Ser Gly					
	385		390		395
Ser Gln Arg Ala Ala Phe Cys Asp His Lys Thr Thr Pro Cys Ser Ser					
	405		410		415
Ala Ile Ile Asn Pro Leu Ser Thr Ala Gly Asn Ser Glu Arg Leu Gln					

420	425	430
Pro Gly Ile Ala Gln Gln Trp Ile Gln Ser Lys Arg Glu Asp Ile Val		
435	440	445
Asn Gln Met Thr Glu Ala Cys Leu Asn Gln Ser Leu Asp Ala Leu Leu		
450	455	460
Ser Arg Asp Leu Ile Met Lys Glu Asp Tyr Glu Leu Val Ser Thr Lys		
465	470	475 480
Pro Thr Arg Thr Ser Lys Val Arg Gln Leu Leu Asp Thr Thr Asp Ile		
485	490	495
Gln Gly Glu Glu Phe Ala Lys Val Ile Val Gln Lys Leu Lys Asp Asn		
500	505	510
Lys Gln Met Gly Leu Gln Pro Tyr Pro Glu Ile Leu Val Val Ser Arg		
515	520	525
Ser Pro Ser Leu Asn Leu Leu Gln Asn Lys Ser Met		
530	535	540

<210> 37
 <211> 1468
 <212> DNA
 <213> Cowpox virus

<220>
 <221> CDS
 <222> (295)..(1320)

<400> 37
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 atatatagaa ttagtataca cgctagatta ttctcaaact cctaattatg acagactacg 180
 tagactgttt atacaagatt gaaaatatat ttctttttat tgagtgggtgg tagttacgga 240
 tatctaatat taatattaga ctatctctat cgtcacacaa caaaatcgat tgcc atg 297
 Met
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gat atc ttc agg gaa atc gca tct tct atg aaa gga gag aat gta ttc 345
 Asp Ile Phe Arg Glu Ile Ala Ser Ser Met Lys Gly Glu Asn Val Phe

5	10	15	
att tct cca ccg tca atc tcg tca gta ttg aca ata ctg tat tat gga	393		
Ile Ser Pro Pro Ser Ile Ser Ser Val Leu Thr Ile Leu Tyr Tyr Gly			
20 25 30			
gct aat gga tcc act gct gaa cag cta tca aaa tat gta gaa aag gag	441		
*Ala Asn Gly Ser Thr Ala Glu Gln Leu Ser Lys Tyr Val Glu Lys Glu			
35 40 45			
gcg gac aag aat aag gat gat atc tca ttc aag tcc atg aat aaa gta	489		
Ala Asp Lys Asn Lys Asp Asp Ile Ser Phe Lys Ser Met Asn Lys Val			
50 55 60 65			
tat ggg cga tat tct gca gtg ttt aaa gat tcc ttt ttg aga aaa att	537		
Tyr Gly Arg Tyr Ser Ala Val Phe Lys Asp Ser Phe Leu Arg Lys Ile			
70 75 80			
gga gat aat ttc caa act gtt gac ttc act gat tgt cgc act gta gat	585		
Gly Asp Asn Phe Gln Thr Val Asp Phe Thr Asp Cys Arg Thr Val Asp			
85 90 95			
gcg atc aac aag tgt gtt gat atc ttc act gag ggg aaa att aat cca	633		
Ala Ile Asn Lys Cys Val Asp Ile Phe Thr Glu Gly Lys Ile Asn Pro			
100 105 110			
cta ttg gat gaa cca ttg tct cca gat acc tgt ctc cta gca att agt	681		
Leu Leu Asp Glu Pro Leu Ser Pro Asp Thr Cys Leu Leu Ala Ile Ser			
115 120 125			
gcc gta tac ttt aaa gca aaa tgg ttg atg cca ttt gaa aag gaa ttt	729		
Ala Val Tyr Phe Lys Ala Lys Trp Leu Met Pro Phe Glu Lys Glu Phe			
130 135 140 145			
acc agt gat tat ccc ttt tac gta tct cca acg gaa atg gta gat gta	777		
Thr Ser Asp Tyr Pro Phe Tyr Val Ser Pro Thr Glu Met Val Asp Val			
150 155 160			
agt atg atg tct atg tac ggc gag gca ttt aat cac gca tct gta aaa	825		
Ser Met Met Ser Met Tyr Gly Glu Ala Phe Asn His Ala Ser Val Lys			
165 170 175			
gaa tca ttc ggc aac ttt tca atc ata gaa ctg cca tat gtt gga gat	873		
Glu Ser Phe Gly Asn Phe Ser Ile Ile Glu Leu Pro Tyr Val Gly Asp			
180 185 190			
act agt atg gtg gta att ctt cca gac aat att gat gga cta gaa tcc	921		
Thr Ser Met Val Val Ile Leu Pro Asp Asn Ile Asp Gly Leu Glu Ser			

195	200	205	
ata gaa caa aat cta aca gat aca aat ttt aag aaa tgg tgt gac tct			969
Ile Glu Gln Asn Leu Thr Asp Thr Asn Phe Lys Lys Trp Cys Asp Ser			
210	215	220	225
atg gat gct atg ttt atc gat gtg cac att ccc aag ttt aag gta aca			1017
Met Asp Ala Met Phe Ile Asp Val His Ile Pro Lys Phe Lys Val Thr			
	230	235	240
ggc tcg tat aat ctg gtg gat gcg cta gta aag ttg gga ctg aca gag			1065
Gly Ser Tyr Asn Leu Val Asp Ala Leu Val Lys Leu Gly Leu Thr Glu			
	245	250	255
gtg ttc ggt tca act gga gat tat agc aat atg tgt aat tca gat gtg			1113
Val Phe Gly Ser Thr Gly Asp Tyr Ser Asn Met Cys Asn Ser Asp Val			
	260	265	270
agt gtc gac gct atg atc cac aaa acg tat ata gat gtc aat gaa gag			1161
Ser Val Asp Ala Met Ile His Lys Thr Tyr Ile Asp Val Asn Glu Glu			
	275	280	285
tat aca gaa gca gct gca gca act tgt gcg ctg gtg gca gac tgt gca			1209
Tyr Thr Glu Ala Ala Ala Ala Thr Cys Ala Leu Val Ala Asp Cys Ala			
	290	295	300
tca aca gtt aca aat gag ttc tgt gca gat cat ccg ttc atc tat gtg			1257
Ser Thr Val Thr Asn Glu Phe Cys Ala Asp His Pro Phe Ile Tyr Val			
	310	315	320
att agg cat gtc gat ggc aaa att ctt ttc gtt ggt aga tat tgc tct			1305
Ile Arg His Val Asp Gly Lys Ile Leu Phe Val Gly Arg Tyr Cys Ser			
	325	330	335
cca aca act aat taa atcacattct taatattaga atattagaat attatatagt			1360
Pro Thr Thr Asn			
	340		
taagattttt actaattggt taaccatttt tttaaaaaaa tagaaaaaaa acatgttata			1420
ttagcgaggg tcgttattct tccaattgca attggtgaaga tgacggcc			1468

<210> 38

<211> 341

<212> PRT

<213> Cowpox virus

<400> 38

Met Asp Ile Phe Arg Glu Ile Ala Ser Ser Met Lys Gly Glu Asn Val
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Phe Ile Ser Pro Pro Ser Ile Ser Ser Val Leu Thr Ile Leu Tyr Tyr
20 25 30

Gly Ala Asn Gly Ser Thr Ala Glu Gln Leu Ser Lys Tyr Val Glu Lys
35 40 45

Glu Ala Asp Lys Asn Lys Asp Asp Ile Ser Phe Lys Ser Met Asn Lys
50 55 60

Val Tyr Gly Arg Tyr Ser Ala Val Phe Lys Asp Ser Phe Leu Arg Lys
65 70 75 80

Ile Gly Asp Asn Phe Gln Thr Val Asp Phe Thr Asp Cys Arg Thr Val
85 90 95

Asp Ala Ile Asn Lys Cys Val Asp Ile Phe Thr Glu Gly Lys Ile Asn
100 105 110

Pro Leu Leu Asp Glu Pro Leu Ser Pro Asp Thr Cys Leu Leu Ala Ile
115 120 125

Ser Ala Val Tyr Phe Lys Ala Lys Trp Leu Met Pro Phe Glu Lys Glu
130 135 140

Phe Thr Ser Asp Tyr Pro Phe Tyr Val Ser Pro Thr Glu Met Val Asp
145 150 155 160

Val Ser Met Met Ser Met Tyr Gly Glu Ala Phe Asn His Ala Ser Val
165 170 175

Lys Glu Ser Phe Gly Asn Phe Ser Ile Ile Glu Leu Pro Tyr Val Gly
180 185 190

Asp Thr Ser Met Val Val Ile Leu Pro Asp Asn Ile Asp Gly Leu Glu
195 200 205

Ser Ile Glu Gln Asn Leu Thr Asp Thr Asn Phe Lys Lys Trp Cys Asp
210 215 220

Ser Met Asp Ala Met Phe Ile Asp Val His Ile Pro Lys Phe Lys Val
225 230 235 240

Thr Gly Ser Tyr Asn Leu Val Asp Ala Leu Val Lys Leu Gly Leu Thr
245 250 255

Glu Val Phe Gly Ser Thr Gly Asp Tyr Ser Asn Met Cys Asn Ser Asp
 260 265 270

Val Ser Val Asp Ala Met Ile His Lys Thr Tyr Ile Asp Val Asn Glu
 275 280 285

Glu Tyr Thr Glu Ala Ala Ala Ala Thr Cys Ala Leu Val Ala Asp Cys
 290 295 300

Ala Ser Thr Val Thr Asn Glu Phe Cys Ala Asp His Pro Phe Ile Tyr
 305 310 315 320

Val Ile Arg His Val Asp Gly Lys Ile Leu Phe Val Gly Arg Tyr Cys
 325 330 335

Ser Pro Thr Thr Asn
 340

<210> 39

<211> 5212

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (2752)..(4566)

<400> 39

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cggcctctgg gcagcaggtt tacaaaggag gaaaacgact tcttctagat ttttttttca 120

gtttcttcta taaatcaaaa catctcaaaa tggagaccta aaatccttaa agggacttag 180

tctaattctcg ggaggtagtt ttgtgcatgg gtaaacaat taagtattaa ctggtgtttt 240

actatccaaa gaatgctaatt ttataaaca tgatcgagtt atataaggta taccataatg 300

agtttgattt tgaatttgat ttgtggaaat aaaggaaaag tgattctagc tggggcatat 360

tgtaaagca tttttttcag agttggccag gcagtctcct actggcacat tctccatta 420

tgtagaatag aaatagtacc tgtgtttggg aaagatttta aaatgagtga cagttatttg 480

gaacaaagag ctaataatca atccactgca aattaaagaa acatgcagat gaaagttttg 540

acacattaaa atactttctac agtgacaaaag aaaaatcaag aacaaagctt tttgatatgt 600
 gcaacaaatt tagaggaagt aaaaagataa atgtgatgat tggtaagaa attatccagt 660
 tattttacaag gccactgata ttttaaactg ccaaaagttt gtttaaattg gctgttaccg 720
 ctgagaatga tgaggatgag aatgatgggt gaaggttaca ttttaggaaa tgaagaaact 780
 tagaaaatta atataaagac agtgatgaat acaagaaga tttttataac aatgtgtaaa 840
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 tatcgactca gaacctcttt actaatgggt agtaaactcat aattgagaaa ttctgaattt 1140
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 aaaaaaactt aacattgagt tgcttcaaca gcatgaaact gagtccaaa gaccaaata 1740
 acaaacacat taatctctga ttattttatt taaatagaat atttaattgt gtaagatcta 1800
 atagtatcat tatacttaag caatcatatt cctgatgatc tatgggaaat aactattatt 1860
 taattaatat tgaaaccagg ttttaagatg tgttagccag tctgttact agtaaactct 1920
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aaaaaatgac taattggaga aaaattgggg atatatcata ttctactgaa ttcaaaatgt 2040
cttcagttgt aaatcttacc attatcttac gtacctctaa gaaataaaag tgcttctaata 2100
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ttttttttcc tggccactaa atttcacaat ttccaaaaag caaaataaac atattctgaa 2280
tatttttgct gtgaaacact tgacagcaga gctttccacc atgaaaagaa gcttcatgag 2340
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actacctccc tagagaaagg ctagtccctt ttcttcccca ttcatttcat t atg aac 2757
Met Asn
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ata gta gaa aac agc ata ttc tta tca aat ttg atg aaa agc gcc tac 2805
Ile Val Glu Asn Ser Ile Phe Leu Ser Asn Leu Met Lys Ser Ala Tyr
5 10 15
acg ttt gaa ctg aaa tac gac ttg tca tgt gaa ctg tac cga atg tct 2853
Thr Phe Glu Leu Lys Tyr Asp Leu Ser Cys Glu Leu Tyr Arg Met Ser
20 25 30
acg tat tcc act ttt cct gct ggg gtt cct gtc tca gaa agg agt ctt 2901
Thr Tyr Ser Thr Phe Pro Ala Gly Val Pro Val Ser Glu Arg Ser Leu
35 40 45 50
gct cgt gct ggt ttc tat tac act ggt gtg aat gac aag gtc aaa tgc 2949
Ala Arg Ala Gly Phe Tyr Tyr Thr Gly Val Asn Asp Lys Val Lys Cys
55 60 65
ttc tgt tgt ggc ctg atg ctg gat aac tgg aaa aga gga gac agt cct 2997
Phe Cys Cys Gly Leu Met Leu Asp Asn Trp Lys Arg Gly Asp Ser Pro
70 75 80

act gaa aag cat aaa aag ttg tat cct agc tgc aga ttc gtt cag agt	3045
Thr Glu Lys His Lys Lys Leu Tyr Pro Ser Cys Arg Phe Val Gln Ser	
85 90 95	
cta aat tcc gtt aac aac ttg gaa gct acc tct cag cct act ttt cct	3093
Leu Asn Ser Val Asn Asn Leu Glu Ala Thr Ser Gln Pro Thr Phe Pro	
100 105 110	
tct tca gta aca aat tcc aca cac tca tta ctt ccg ggt aca gaa aac	3141
Ser Ser Val Thr Asn Ser Thr His Ser Leu Leu Pro Gly Thr Glu Asn	
115 120 125 130	
agt gga tat ttc cgt ggc tct tat tca aac tct cca tca aat cct gta	3189
Ser Gly Tyr Phe Arg Gly Ser Tyr Ser Asn Ser Pro Ser Asn Pro Val	
135 140 145	
aac tcc aga gca aat caa gat ttt tct gcc ttg atg aga agt tcc tac	3237
Asn Ser Arg Ala Asn Gln Asp Phe Ser Ala Leu Met Arg Ser Ser Tyr	
150 155 160	
cac tgt gca atg aat aac gaa aat gcc aga tta ctt act ttt cag aca	3285
His Cys Ala Met Asn Asn Glu Asn Ala Arg Leu Leu Thr Phe Gln Thr	
165 170 175	
tgg cca ttg act ttt ctg tct cca aca gat ctg gca aaa gca ggc ttt	3333
Trp Pro Leu Thr Phe Leu Ser Pro Thr Asp Leu Ala Lys Ala Gly Phe	
180 185 190	
tac tac ata gga cct gga gac aga gtg gct tgc ttt gcc tgt ggt gga	3381
Tyr Tyr Ile Gly Pro Gly Asp Arg Val Ala Cys Phe Ala Cys Gly Gly	
195 200 205 210	
aaa ttg agc aat tgg gaa ccg aag gat aat gct atg tca gaa cac ctg	3429
Lys Leu Ser Asn Trp Glu Pro Lys Asp Asn Ala Met Ser Glu His Leu	
215 220 225	
aga cat ttt ccc aaa tgc cca ttt ata gaa aat cag ctt caa gac act	3477
Arg His Phe Pro Lys Cys Pro Phe Ile Glu Asn Gln Leu Gln Asp Thr	
230 235 240	
tca aga tac aca gtt tct aat ctg agc atg cag aca cat gca gcc cgc	3525
Ser Arg Tyr Thr Val Ser Asn Leu Ser Met Gln Thr His Ala Ala Arg	
245 250 255	
ttt aaa aca ttc ttt aac tgg ccc tct agt gtt cta gtt aat cct gag	3573
Phe Lys Thr Phe Phe Asn Trp Pro Ser Ser Val Leu Val Asn Pro Glu	
260 265 270	

agt cta cta act gcc gga att att aat gaa caa gaa cat gat gtt att 4197
 Ser Leu Leu Thr Ala Gly Ile Ile Asn Glu Gln Glu His Asp Val Ile
 470 475 480

aaa cag aag aca cag acg tct tta caa gca aga gaa ctg att gat acg 4245
 Lys Gln Lys Thr Gln Thr Ser Leu Gln Ala Arg Glu Leu Ile Asp Thr
 485 490 495

att tta gta aaa gga aat att gca gcc act gta ttc aga aac tct ctg 4293
 Ile Leu Val Lys Gly Asn Ile Ala Ala Thr Val Phe Arg Asn Ser Leu
 500 505 510

caa gaa gct gaa gct gtg tta tat gag cat tta ttt gtg caa cag gac 4341
 Gln Glu Ala Glu Ala Val Leu Tyr Glu His Leu Phe Val Gln Gln Asp
 515 520 525 530

ata aaa tat att ccc aca gaa gat gtt tca gat cta cca gtg gaa gaa 4389
 Ile Lys Tyr Ile Pro Thr Glu Asp Val Ser Asp Leu Pro Val Glu Glu
 535 540 545

caa ttg cgg aga cta caa gaa gaa aga aca tgt aaa gtg tgt atg gac 4437
 Gln Leu Arg Arg Leu Gln Glu Glu Arg Thr Cys Lys Val Cys Met Asp
 550 555 560

aaa gaa gtg tcc ata gtg ttt att cct tgt ggt cat cta gta gta tgc 4485
 Lys Glu Val Ser Ile Val Phe Ile Pro Cys Gly His Leu Val Val Cys
 565 570 575

aaa gat tgt gct cct tct tta aga aag tgt cct att tgt agg agt aca 4533
 Lys Asp Cys Ala Pro Ser Leu Arg Lys Cys Pro Ile Cys Arg Ser Thr
 580 585 590

atc aag ggt aca gtt cgt aca ttt ctt tca tga agaagaacca aaacatcatc 4586
 Ile Lys Gly Thr Val Arg Thr Phe Leu Ser
 595 600 605

taaacttttag aattaattta ttaaattgtat tataacttta acttttatcc taatttggtt 4646

tccttaaaat ttttatttat ttacaactca aaaaacattg ttttgtgtaa catatttata 4706

tatgtatcta aaccatatga acatatattt tttagaaact aagagaatga taggcttttg 4766

ttcttatgaa cgaaaaagag gtagcactac aaacacaata ttcaatcaaa atttcagcat 4826

tattgaaatt gtaagtgaag taaaacttaa gatatttgag ttaaccttta agaatttttaa 4886

atattttggc attgtactaa taccgggaac atgaagccag gtgtggtggt atgtgcctgt 4946

agtcccaggc tgaggcaaga gaattacttg agcccaggag tttgaatcca tcctgggcag 5006
 catactgaga ccttgccttt aaaaacaaac agaacaaaaa caaaacacca gggacacatt 5066
 tctctgtctt ttttgatcag tgtcctatac atcgaagggtg tgcataatg ttgaatgaca 5126
 ttttagggac atggtgtttt tataaagaat tctgtgagaa aaaatttaat aaagcaacaa 5186
 aaattactct taaaaaaaaa aaaaaa 5212

<210> 40
 <211> 604
 <212> PRT
 <213> Homo sapiens

<400> 40

Met	Asn	Ile	Val	Glu	Asn	Ser	Ile	Phe	Leu	Ser	Asn	Leu	Met	Lys	Ser
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Ala	Tyr	Thr	Phe	Glu	Leu	Lys	Tyr	Asp	Leu	Ser	Cys	Glu	Leu	Tyr	Arg
			20					25					30		
Met	Ser	Thr	Tyr	Ser	Thr	Phe	Pro	Ala	Gly	Val	Pro	Val	Ser	Glu	Arg
		35					40					45			
Ser	Leu	Ala	Arg	Ala	Gly	Phe	Tyr	Tyr	Thr	Gly	Val	Asn	Asp	Lys	Val
	50					55						60			
Lys	Cys	Phe	Cys	Cys	Gly	Leu	Met	Leu	Asp	Asn	Trp	Lys	Arg	Gly	Asp
65					70					75				80	
Ser	Pro	Thr	Glu	Lys	His	Lys	Lys	Leu	Tyr	Pro	Ser	Cys	Arg	Phe	Val
				85					90					95	
Gln	Ser	Leu	Asn	Ser	Val	Asn	Asn	Leu	Glu	Ala	Thr	Ser	Gln	Pro	Thr
		100						105					110		
Phe	Pro	Ser	Ser	Val	Thr	Asn	Ser	Thr	His	Ser	Leu	Leu	Pro	Gly	Thr
		115						120					125		
Glu	Asn	Ser	Gly	Tyr	Phe	Arg	Gly	Ser	Tyr	Ser	Asn	Ser	Pro	Ser	Asn
	130					135					140				
Pro	Val	Asn	Ser	Arg	Ala	Asn	Gln	Asp	Phe	Ser	Ala	Leu	Met	Arg	Ser
145					150					155				160	
Ser	Tyr	His	Cys	Ala	Met	Asn	Asn	Glu	Asn	Ala	Arg	Leu	Leu	Thr	Phe

165	170	175
Gln Thr Trp Pro Leu Thr Phe Leu Ser Pro Thr Asp Leu Ala Lys Ala		
180	185	190
Gly Phe Tyr Tyr Ile Gly Pro Gly Asp Arg Val Ala Cys Phe Ala Cys		
195	200	205
Gly Gly Lys Leu Ser Asn Trp Glu Pro Lys Asp Asn Ala Met Ser Glu		
210	215	220
His Leu Arg His Phe Pro Lys Cys Pro Phe Ile Glu Asn Gln Leu Gln		
225	230	235 240
Asp Thr Ser Arg Tyr Thr Val Ser Asn Leu Ser Met Gln Thr His Ala		
245	250	255
Ala Arg Phe Lys Thr Phe Phe Asn Trp Pro Ser Ser Val Leu Val Asn		
260	265	270
Pro Glu Gln Leu Ala Ser Ala Gly Phe Tyr Tyr Val Gly Asn Ser Asp		
275	280	285
Asp Val Lys Cys Phe Cys Cys Asp Gly Gly Leu Arg Cys Trp Glu Ser		
290	295	300
Gly Asp Asp Pro Trp Val Gln His Ala Lys Trp Phe Pro Arg Cys Glu		
305	310	315 320
Tyr Leu Ile Arg Ile Lys Gly Gln Glu Phe Ile Arg Gln Val Gln Ala		
325	330	335
Ser Tyr Pro His Leu Leu Glu Gln Leu Leu Ser Thr Ser Asp Ser Pro		
340	345	350
Gly Asp Glu Asn Ala Glu Ser Ser Ile Ile His Phe Glu Pro Gly Glu		
355	360	365
Asp His Ser Glu Asp Ala Ile Met Met Asn Thr Pro Val Ile Asn Ala		
370	375	380
Ala Val Glu Met Gly Phe Ser Arg Ser Leu Val Lys Gln Thr Val Gln		
385	390	395 400
Arg Lys Ile Leu Ala Thr Gly Glu Asn Tyr Arg Leu Val Asn Asp Leu		
405	410	415
Val Leu Asp Leu Leu Asn Ala Glu Asp Glu Ile Arg Glu Glu Glu Arg		

420	425	430
Glu Arg Ala Thr Glu Glu Lys Glu Ser Asn Asp Leu Leu Leu Ile Arg		
435	440	445
Lys Asn Arg Met Ala Leu Phe Gln His Leu Thr Cys Val Ile Pro Ile		
450	455	460
Leu Asp Ser Leu Leu Thr Ala Gly Ile Ile Asn Glu Gln Glu His Asp		
465	470	475 480
Val Ile Lys Gln Lys Thr Gln Thr Ser Leu Gln Ala Arg Glu Leu Ile		
485	490	495
Asp Thr Ile Leu Val Lys Gly Asn Ile Ala Ala Thr Val Phe Arg Asn		
500	505	510
Ser Leu Gln Glu Ala Glu Ala Val Leu Tyr Glu His Leu Phe Val Gln		
515	520	525
Gln Asp Ile Lys Tyr Ile Pro Thr Glu Asp Val Ser Asp Leu Pro Val		
530	535	540
Glu Glu Gln Leu Arg Arg Leu Gln Glu Glu Arg Thr Cys Lys Val Cys		
545	550	555 560
Met Asp Lys Glu Val Ser Ile Val Phe Ile Pro Cys Gly His Leu Val		
565	570	575
Val Cys Lys Asp Cys Ala Pro Ser Leu Arg Lys Cys Pro Ile Cys Arg		
580	585	590
Ser Thr Ile Lys Gly Thr Val Arg Thr Phe Leu Ser		
595	600	

<210> 41

<211> 1034

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (195)..(1034)

<400> 41

gacgcttctg gggagtgagg gaagcggttt acgagtgact tggctggagc ctcaggggcg 60

ggcactggca cggaacacac cctgaggcca gccctggctg cccaggcgga gctgcctctt 120
 ctccccgctggg ttggtggacc cgctcagtag ggagttgggg aagctctttc acttcggagg 180
 attgctcaac aacc atg ctg ggc atc tgg acc ctc cta cct ctg gtt ctt 230
 Met Leu Gly Ile Trp Thr Leu Leu Pro Leu Val Leu
 1 5 10
 acg tct gtt gct aga tta tcg tcc aaa agt gtt aat gcc caa gtg act 278
 Thr Ser Val Ala Arg Leu Ser Ser Lys Ser Val Asn Ala Gln Val Thr
 15 20 25
 gac atc aac tcc aag gga ttg gaa ttg agg aag act gtt act aca gtt 326
 Asp Ile Asn Ser Lys Gly Leu Glu Leu Arg Lys Thr Val Thr Thr Val
 30 35 40
 gag act cag aac ttg gaa ggc ctg cat cat gat ggc caa ttc tgc cat 374
 Glu Thr Gln Asn Leu Glu Gly Leu His His Asp Gly Gln Phe Cys His
 45 50 55 60
 aag ccc tgt cct cca ggt gaa agg aaa gct agg gac tgc aca gtc aat 422
 Lys Pro Cys Pro Pro Gly Glu Arg Lys Ala Arg Asp Cys Thr Val Asn
 65 70 75
 ggg gat gaa cca gac tgc gtg ccc tgc caa gaa ggg aag gag tac aca 470
 Gly Asp Glu Pro Asp Cys Val Pro Cys Gln Glu Gly Lys Glu Tyr Thr
 80 85 90
 gac aaa gcc cat ttt tct tcc aaa tgc aga aga tgt aga ttg tgt gat 518
 Asp Lys Ala His Phe Ser Ser Lys Cys Arg Arg Cys Arg Leu Cys Asp
 95 100 105
 gaa gga cat ggc tta gaa gtg gaa ata aac tgc acc cgg acc cag aat 566
 Glu Gly His Gly Leu Glu Val Glu Ile Asn Cys Thr Arg Thr Gln Asn
 110 115 120
 acc aag tgc aga tgt aaa cca aac ttt ttt tgt aac tct act gta tgt 614
 Thr Lys Cys Arg Cys Lys Pro Asn Phe Phe Cys Asn Ser Thr Val Cys
 125 130 135 140
 gaa cac tgt gac cct tgc acc aaa tgt gaa cat gga atc atc aag gaa 662
 Glu His Cys Asp Pro Cys Thr Lys Cys Glu His Gly Ile Ile Lys Glu
 145 150 155
 tgc aca ctc acc agc aac acc aag tgc aaa gag gaa gga tcc aga tct 710
 Cys Thr Leu Thr Ser Asn Thr Lys Cys Lys Glu Glu Gly Ser Arg Ser
 160 165 170

aac ttg ggg tgg ctt tgt ctt ctt ctt ttg cca att cca cta att gtt 758
 Asn Leu Gly Trp Leu Cys Leu Leu Leu Leu Pro Ile Pro Leu Ile Val
 175 180 185

tgg gtg aag aga aag gaa gta cag aaa aca tgc aga aag cac aga aag 806
 Trp Val Lys Arg Lys Glu Val Gln Lys Thr Cys Arg Lys His Arg Lys
 190 195 200

gaa aac caa ggt tct cat gaa tct cca acc tta aat cct gaa aca gtg 854
 Glu Asn Gln Gly Ser His Glu Ser Pro Thr Leu Asn Pro Glu Thr Val
 205 210 215 220

gca ata aat tta tct gat gtt gac ttg agt aaa tat atc acc act att 902
 Ala Ile Asn Leu Ser Asp Val Asp Leu Ser Lys Tyr Ile Thr Thr Ile
 225 230 235

gct gga gtc atg aca cta agt caa gtt aaa ggc ttt gtt cga aag aat 950
 Ala Gly Val Met Thr Leu Ser Gln Val Lys Gly Phe Val Arg Lys Asn
 240 245 250

ggt gtc aat gaa gcc aaa ata gat gag atc aag aat gac aat gtc caa 998
 Gly Val Asn Glu Ala Lys Ile Asp Glu Ile Lys Asn Asp Asn Val Gln
 255 260 265

gac aca gca gaa cag aaa gtt caa ctg ctt cgt aat 1034
 Asp Thr Ala Glu Gln Lys Val Gln Leu Leu Arg Asn
 270 275 280

<210> 42

<211> 280

<212> PRT

<213> Homo sapiens

<400> 42

Met Leu Gly Ile Trp Thr Leu Leu Pro Leu Val Leu Thr Ser Val Ala
 1 5 10 15

Arg Leu Ser Ser Lys Ser Val Asn Ala Gln Val Thr Asp Ile Asn Ser
 20 25 30

Lys Gly Leu Glu Leu Arg Lys Thr Val Thr Thr Val Glu Thr Gln Asn
 35 40 45

Leu Glu Gly Leu His His Asp Gly Gln Phe Cys His Lys Pro Cys Pro
 50 55 60

Pro Gly Glu Arg Lys Ala Arg Asp Cys Thr Val Asn Gly Asp Glu Pro

65		70		75		80
Asp Cys Val Pro Cys Gln Glu Gly Lys Glu Tyr Thr Asp Lys Ala His						
	85		90		95	
Phe Ser Ser Lys Cys Arg Arg Cys Arg Leu Cys Asp Glu Gly His Gly						
	100		105		110	
Leu Glu Val Glu Ile Asn Cys Thr Arg Thr Gln Asn Thr Lys Cys Arg						
	115		120		125	
Cys Lys Pro Asn Phe Phe Cys Asn Ser Thr Val Cys Glu His Cys Asp						
	130		135		140	
Pro Cys Thr Lys Cys Glu His Gly Ile Ile Lys Glu Cys Thr Leu Thr						
145		150		155		160
Ser Asn Thr Lys Cys Lys Glu Glu Gly Ser Arg Ser Asn Leu Gly Trp						
	165		170		175	
Leu Cys Leu Leu Leu Leu Pro Ile Pro Leu Ile Val Trp Val Lys Arg						
	180		185		190	
Lys Glu Val Gln Lys Thr Cys Arg Lys His Arg Lys Glu Asn Gln Gly						
	195		200		205	
Ser His Glu Ser Pro Thr Leu Asn Pro Glu Thr Val Ala Ile Asn Leu						
	210		215		220	
Ser Asp Val Asp Leu Ser Lys Tyr Ile Thr Thr Ile Ala Gly Val Met						
225		230		235		240
Thr Leu Ser Gln Val Lys Gly Phe Val Arg Lys Asn Gly Val Asn Glu						
	245		250		255	
Ala Lys Ile Asp Glu Ile Lys Asn Asp Asn Val Gln Asp Thr Ala Glu						
	260		265		270	
Gln Lys Val Gln Leu Leu Arg Asn						
	275		280			

<210> 43

<211> 2056

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (413)..(1750)

<400> 43

cgagtctcaa ctaaaagga ctcccggagc taggggtggg gactcggcct cacacagtga 60

gtgccgggcta ttggactttt gtccagtga acgtgagaca acaaggacca cgggaggagg 120

tgtaggagag aagcgccgcg aacagcgatc gcccagcacc aagtccgctt ccaggctttc 180

ggttttctttg cctccatctt ggggtgcgcct tcccggcgtc taggggagcg aaggctgagg 240

tggcagcggc aggagagtcc ggccgcgaca ggacgaactc cccactgga aaggattctg 300

aaagaaatga agtcagccct cagaaatgaa gttgactgcc tgctggcttt ctgttgactg 360

gcccggagct gtactgcaag acccttgtga gcttccctag tctaagagta gg atg tct 418

Met Ser

1

gct gaa gtc atc cat cag gtt gaa gaa gca ctt gat aca gat gag aag 466

Ala Glu Val Ile His Gln Val Glu Glu Ala Leu Asp Thr Asp Glu Lys

5

10

15

gag atg ctg ctc ttt ttg tgc cgg gat gtt gct ata gat gtg gtt cca 514

Glu Met Leu Leu Phe Leu Cys Arg Asp Val Ala Ile Asp Val Val Pro

20

25

30

cct aat gtc agg gac ctt ctg gat att tta cgg gaa aga ggt aag ctg 562

Pro Asn Val Arg Asp Leu Leu Asp Ile Leu Arg Glu Arg Gly Lys Leu

35

40

45

50

tct gtc ggg gac ttg gct gaa ctg ctc tac aga gtg agg cga ttt gac 610

Ser Val Gly Asp Leu Ala Glu Leu Leu Tyr Arg Val Arg Arg Phe Asp

55

60

65

ctg ctc aaa cgt atc ttg aag atg gac aga aaa gct gtg gag acc cac 658

Leu Leu Lys Arg Ile Leu Lys Met Asp Arg Lys Ala Val Glu Thr His

70

75

80

ctg ctc agg aac cct cac ctt gtt tcg gac tat aga gtg ctg atg gca 706

Leu Leu Arg Asn Pro His Leu Val Ser Asp Tyr Arg Val Leu Met Ala

85

90

95

gag att ggt gag gat ttg gat aaa tct gat gtg tcc tca tta att ttc 754

Glu Ile Gly Glu Asp Leu Asp Lys Ser Asp Val Ser Ser Leu Ile Phe

100

105

110

ctc atg aag gat tac atg ggc cga ggc aag ata agc aag gag aag agt	802
Leu Met Lys Asp Tyr Met Gly Arg Gly Lys Ile Ser Lys Glu Lys Ser	
115 120 125 130	
ttc ttg gac ctt gtg gtt gag ttg gag aaa cta aat ctg gtt gcc cca	850
Phe Leu Asp Leu Val Val Glu Leu Glu Lys Leu Asn Leu Val Ala Pro	
135 140 145	
gat caa ctg gat tta tta gaa aaa tgc cta aag aac atc cac aga ata	898
Asp Gln Leu Asp Leu Leu Glu Lys Cys Leu Lys Asn Ile His Arg Ile	
150 155 160	
gac ctg aag aca aaa atc cag aag tac aag cag tct gtt caa gga gca	946
Asp Leu Lys Thr Lys Ile Gln Lys Tyr Lys Gln Ser Val Gln Gly Ala	
165 170 175	
ggg aca agt tac agg aat gtt ctc caa gca gca atc caa aag agt ctc	994
Gly Thr Ser Tyr Arg Asn Val Leu Gln Ala Ala Ile Gln Lys Ser Leu	
180 185 190	
aag gat cct tca aat aac ttc agg agc ata cct gaa gag aga tac aag	1042
Lys Asp Pro Ser Asn Asn Phe Arg Ser Ile Pro Glu Glu Arg Tyr Lys	
195 200 205 210	
atg aag agc aag ccc cta gga atc tgc ctg ata atc gat tgc att ggc	1090
Met Lys Ser Lys Pro Leu Gly Ile Cys Leu Ile Ile Asp Cys Ile Gly	
215 220 225	
aat gag aca gag ctt ctt cga gac acc ttc act tcc ctg ggc tat gaa	1138
Asn Glu Thr Glu Leu Leu Arg Asp Thr Phe Thr Ser Leu Gly Tyr Glu	
230 235 240	
gtc cag aaa ttc ttg cat ctc agt atg cat ggt ata tcc cag att ctt	1186
Val Gln Lys Phe Leu His Leu Ser Met His Gly Ile Ser Gln Ile Leu	
245 250 255	
ggc caa ttt gcc tgt atg ccc gag cac cga gac tac gac agc ttt gtg	1234
Gly Gln Phe Ala Cys Met Pro Glu His Arg Asp Tyr Asp Ser Phe Val	
260 265 270	
tgt gtc ctg gtg agc cga gga ggc tcc cag agt gtg tat ggt gtg gat	1282
Cys Val Leu Val Ser Arg Gly Gly Ser Gln Ser Val Tyr Gly Val Asp	
275 280 285 290	
cag act cac tca ggg ctc ccc ctg cat cac atc agg agg atg ttc atg	1330
Gln Thr His Ser Gly Leu Pro Leu His His Ile Arg Arg Met Phe Met	
295 300 305	

gga gat tca tgc cct tat cta gca ggg aag cca aag atg ttt ttt att 1378
 Gly Asp Ser Cys Pro Tyr Leu Ala Gly Lys Pro Lys Met Phe Phe Ile
 310 315 320

cag aac tat gtg gtg tca gag ggc cag ctg gag gac agc agc ctc ttg 1426
 Gln Asn Tyr Val Val Ser Glu Gly Gln Leu Glu Asp Ser Ser Leu Leu
 325 330 335

gag gtg gat ggg cca gcg atg aag aat gtg gaa ttc aag gct cag aag 1474
 Glu Val Asp Gly Pro Ala Met Lys Asn Val Glu Phe Lys Ala Gln Lys
 340 345 350

cga ggg ctg tgc aca gtt cac cga gaa gct gac ttc ttc tgg agc ctg 1522
 Arg Gly Leu Cys Thr Val His Arg Glu Ala Asp Phe Phe Trp Ser Leu
 355 360 365 370

tgt act gcg gac atg tcc ctg ctg gag cag tct cac agc tca ccg tcc 1570
 Cys Thr Ala Asp Met Ser Leu Leu Glu Gln Ser His Ser Ser Pro Ser
 375 380 385

ctg tac ctg cag tgc ctc tcc cag aaa ctg aga caa gaa aga aaa cgc 1618
 Leu Tyr Leu Gln Cys Leu Ser Gln Lys Leu Arg Gln Glu Arg Lys Arg
 390 395 400

cca ctc ctg gat ctt cac att gaa ctc aat ggc tac atg tat gat tgg 1666
 Pro Leu Leu Asp Leu His Ile Glu Leu Asn Gly Tyr Met Tyr Asp Trp
 405 410 415

aac agc aga gtt tct gcc aag gag aaa tat tat gtt tgg ctg cag cac 1714
 Asn Ser Arg Val Ser Ala Lys Glu Lys Tyr Tyr Val Trp Leu Gln His
 420 425 430

act ctg aga aag aaa ctt atc ctc tcc tac aca taa gaaacaaaa 1760
 Thr Leu Arg Lys Lys Leu Ile Leu Ser Tyr Thr
 435 440 445

ggctgggcgt agtgggtcac acctgtaatc ccagcacttt gggaggccaa ggagggcaga 1820

tcacttcagg tcaggagttc gagaccagcc tggccaacat ggtaaagcgt gtccttagta 1880

aaaatacaaaa aattagctgg gtgtgggtgt gggtagctgt attcccagtt acttgggagg 1940

ctgaggtggg aggatctttt gaaccaggga gttcagggtc atagcatgct gtgattgtgc 2000

ctacgaatag ccactgcata ccaacctggg caatatagca agatcccatc tcttta 2056

<210> 44

<211> 445

<212> PRT

<213> Homo sapiens

<400> 44

Met Ser Ala Glu Val Ile His Gln Val Glu Glu Ala Leu Asp Thr Asp
1 5 10 15

Glu Lys Glu Met Leu Leu Phe Leu Cys Arg Asp Val Ala Ile Asp Val
20 25 30

Val Pro Pro Asn Val Arg Asp Leu Leu Asp Ile Leu Arg Glu Arg Gly
35 40 45

Lys Leu Ser Val Gly Asp Leu Ala Glu Leu Leu Tyr Arg Val Arg Arg
50 55 60

Phe Asp Leu Leu Lys Arg Ile Leu Lys Met Asp Arg Lys Ala Val Glu
65 70 75 80

Thr His Leu Leu Arg Asn Pro His Leu Val Ser Asp Tyr Arg Val Leu
85 90 95

Met Ala Glu Ile Gly Glu Asp Leu Asp Lys Ser Asp Val Ser Ser Leu
100 105 110

Ile Phe Leu Met Lys Asp Tyr Met Gly Arg Gly Lys Ile Ser Lys Glu
115 120 125

Lys Ser Phe Leu Asp Leu Val Val Glu Leu Glu Lys Leu Asn Leu Val
130 135 140

Ala Pro Asp Gln Leu Asp Leu Leu Glu Lys Cys Leu Lys Asn Ile His
145 150 155 160

Arg Ile Asp Leu Lys Thr Lys Ile Gln Lys Tyr Lys Gln Ser Val Gln
165 170 175

Gly Ala Gly Thr Ser Tyr Arg Asn Val Leu Gln Ala Ala Ile Gln Lys
180 185 190

Ser Leu Lys Asp Pro Ser Asn Asn Phe Arg Ser Ile Pro Glu Glu Arg
195 200 205

Tyr Lys Met Lys Ser Lys Pro Leu Gly Ile Cys Leu Ile Ile Asp Cys
210 215 220

Ile Gly Asn Glu Thr Glu Leu Leu Arg Asp Thr Phe Thr Ser Leu Gly

225	230	235	240
Tyr Glu Val Gln Lys Phe Leu His Leu Ser Met His Gly Ile Ser Gln			
245	250	255	
Ile Leu Gly Gln Phe Ala Cys Met Pro Glu His Arg Asp Tyr Asp Ser			
260	265	270	
Phe Val Cys Val Leu Val Ser Arg Gly Gly Ser Gln Ser Val Tyr Gly			
275	280	285	
Val Asp Gln Thr His Ser Gly Leu Pro Leu His His Ile Arg Arg Met			
290	295	300	
Phe Met Gly Asp Ser Cys Pro Tyr Leu Ala Gly Lys Pro Lys Met Phe			
305	310	315	320
Phe Ile Gln Asn Tyr Val Val Ser Glu Gly Gln Leu Glu Asp Ser Ser			
325	330	335	
Leu Leu Glu Val Asp Gly Pro Ala Met Lys Asn Val Glu Phe Lys Ala			
340	345	350	
Gln Lys Arg Gly Leu Cys Thr Val His Arg Glu Ala Asp Phe Phe Trp			
355	360	365	
Ser Leu Cys Thr Ala Asp Met Ser Leu Leu Glu Gln Ser His Ser Ser			
370	375	380	
Pro Ser Leu Tyr Leu Gln Cys Leu Ser Gln Lys Leu Arg Gln Glu Arg			
385	390	395	400
Lys Arg Pro Leu Leu Asp Leu His Ile Glu Leu Asn Gly Tyr Met Tyr			
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Arg Glu Ile Val Met Lys Tyr Ile His Tyr Lys Leu Ser Gln Arg Gly
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Tyr Glu Trp Asp Ala Gly Asp Val Gly Ala Ala Pro Pro Gly Ala Ala
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Pro Ala Pro Gly Ile Phe Ser Ser Gln Pro Gly His Thr Pro His Pro
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145 150 155 160

Ser Val Asn Arg Glu Met Ser Pro Leu Val Asp Asn Ile Ala Leu Trp
165 170 175

Met Thr Glu Tyr Leu Asn Arg His Leu His Thr Trp Ile Gln Asp Asn
180 185 190

Gly Gly Trp Asp Ala Phe Val Glu Leu Tyr Gly Pro Ser Met Arg Pro
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Met Ser Gln Ser Asn Arg Glu Leu Val Val Asp Phe
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ctc tcc tac aag ctt tcc cag aaa gga tac agc tgg agt cag ttt agt 218
Leu Ser Tyr Lys Leu Ser Gln Lys Gly Tyr Ser Trp Ser Gln Phe Ser
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Met Glu Thr Pro Ser Ala Ile Asn Gly Asn Pro Ser Trp His Leu Ala	
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Asp Ser Pro Ala Val Asn Gly Ala Thr Ala His Ser Ser Ser Leu Asp	
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Ala Arg Glu Val Ile Pro Met Ala Ala Val Lys Gln Ala Leu Arg Glu	
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Ala Gly Asp Glu Phe Glu Leu Arg Tyr Arg Arg Ala Phe Ser Asp Leu	
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aca tcc cag ctc cac atc acc cca ggg aca gca tat cag agc ttt gaa	506
Thr Ser Gln Leu His Ile Thr Pro Gly Thr Ala Tyr Gln Ser Phe Glu	
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cag gta gtg aat gaa ctc ttc cgg gat ggg gta aac tgg ggt cgc att	554
Gln Val Val Asn Glu Leu Phe Arg Asp Gly Val Asn Trp Gly Arg Ile	
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Val Ala Phe Phe Ser Phe Gly Gly Ala Leu Cys Val Glu Ser Val Asp	
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Lys Glu Met Gln Val Leu Val Ser Arg Ile Ala Ala Trp Met Ala Thr	
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Tyr Leu Asn Asp His Leu Glu Pro Trp Ile Gln Glu Asn Gly Gly Trp	
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gat act ttt gtg gaa ctc tat ggg aac aat gca gca gcc gag agc cga	746
Asp Thr Phe Val Glu Leu Tyr Gly Asn Asn Ala Ala Ala Glu Ser Arg	
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Lys Gly Gln Glu Arg Phe Asn Arg Trp Phe Leu Thr Gly Met Thr Val	
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gcc ggc gtg gtt ctg ctg ggc tca ctc ttc agt cgg aaa tga	836

Ala Gly Val Val Leu Leu Gly Ser Leu Phe Ser Arg Lys

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230

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926

<210> 48

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<212> PRT

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Asn Arg Thr Glu Ala Pro Glu Gly Thr Glu Ser Glu Met Glu Thr Pro

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40

45

Ser Ala Ile Asn Gly Asn Pro Ser Trp His Leu Ala Asp Ser Pro Ala

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55

60

Val Asn Gly Ala Thr Ala His Ser Ser Ser Leu Asp Ala Arg Glu Val

65

70

75

80

Ile Pro Met Ala Ala Val Lys Gln Ala Leu Arg Glu Ala Gly Asp Glu

85

90

95

Phe Glu Leu Arg Tyr Arg Arg Ala Phe Ser Asp Leu Thr Ser Gln Leu

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105

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His Ile Thr Pro Gly Thr Ala Tyr Gln Ser Phe Glu Gln Val Val Asn

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120

125

Glu Leu Phe Arg Asp Gly Val Asn Trp Gly Arg Ile Val Ala Phe Phe

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Ser Phe Gly Gly Ala Leu Cys Val Glu Ser Val Asp Lys Glu Met Gln

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Val Leu Val Ser Arg Ile Ala Ala Trp Met Ala Thr Tyr Leu Asn Asp

165

170

175

His Leu Glu Pro Trp Ile Gln Glu Asn Gly Gly Trp Asp Thr Phe Val

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Glu Leu Tyr Gly Asn Asn Ala Ala Ala Glu Ser Arg Lys Gly Gln Glu		
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atc agg cag cgg gga cag aga atc ttg aat tac tgg ctt cta cag cca			1994
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Pro Pro Ser Glu Glu Glu Leu Asp			
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Glu Glu Phe Glu Asn Ile Phe Ala Asp Cys Ser Gly Leu Leu Asp Ser
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Leu Asn Leu Gly His Gln Ser Leu Phe Gln Glu Arg Val Leu His Ser
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Leu Asp Phe Ser Ser Pro Gly Arg Thr Thr Ala Gly Val Ala Phe Val
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Tyr Ile Leu Asp Phe Ala Ala Met His Leu Trp Arg Ala Trp Ile Arg
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Gln Arg Gly Gln Arg Ile Leu Asn Tyr Trp Leu Leu Gln Pro Ala Ala
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Pro Gly Leu Leu Arg Leu His Arg Gln Thr Ser Met Leu Glu Glu Glu
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Ser Glu Glu Glu Leu Asp
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